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-08-102-896-3
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1 to the score of the result being printed,
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10.296 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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USA

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COMPUTER READABLE FORM:

ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,534

FILING DATE: 14-SEP-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: NO. 6022855nan, Kevin E

REGISTRATION NUMBER: 35,303

REPRENCE/DOCKET NUMBER: 92,448-D

TELEPHONE: 312-913-0001

TELEPHONE: 312-913-0002
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
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Best Local Similarity 100.0
Matches 4; Conservative
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                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Thomas, Garry
APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
TITLE OF INVENTION: Methods and Reagents for Inhibiting
TITLE OF INVENTION: Purin Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING $YSTEM: PC-DOS/MS-DOS
SOFTWARE: 'PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: Illinois
                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: NO. 560420.nan, Kevin B
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,448
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
                                                                                                                                                               Sequence 10, Application US/08002202 Patent No. 5604201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 310-221-5317
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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Best Local Similarity
Matches 4; Conserv
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Gaps

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0; Indels

Score 21; DB 3; Length 4; Pred. No. 4.1e+05;

100.0%; Scor. 100.0%; Pred. No. ... 0; Mismatches

10:

amino acid

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APPLICANT: Thomas, Gary
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Relson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
ZIP: 60606
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURENT APPLICATION DATA:: US/08/481,534
FILING DATE: 14-SEP-1995
CLASSIFICATION: 530
ATTORNEY/ AGENT INFORMATION:
NAME: No. 6022855nan, Kevin E
NAME: NO. 6022855nan, Kevin E
                Sequence 15, Application US/08481534 Patent No. 6022855
                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       IL
US-08-481-534-15
                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: C
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GENERAL INFORMATION:

APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Hayflick, Joel S
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Endoprotease

CORRESPONDENCE ADDRESS:

Sequence 10, Application US/08481534 Patent No. 6022855

RESULT 2 US-08-481-534-10

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APPLICANT: Thomas, Garry
APPLICANT: Thomas, Garry
APPLICANT: Thomas, Earle D
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
ITILE OF INVENTION: Methods and Reagents for Inhibiting
ITILE OF INVENTION: Methods and Reagents for Inhibiting
ITILE OF INVENTION: Furin Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
COUNTRY: USA
ITILE OF SEQUENCES
COUNTRY: USA
ITILE OF STATES
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 00-JAN-1993
CLASSIFICATION: 514
ATTORNEY/AGRAT INPORMATION:
NAME: NO. 5604201nan, Kevin E
REGISTRATION NUMBER: 35,30003
REPERENCE/DOCKET NUMBER: 35,30003
REPERENCE/DOCKET NUMBER: 32,448
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Sequence 22, Application US/08726160

Patent No. 5734016

GENERAL INFORMATION:

APPLICANT: LEVENS, DAVID L., DUNCAN,

TITLE OF INVENTION: NOVEL FUSE BINDING

TITLE OF INVENTION: POPTEIN AND CONA THEREFOR

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Le
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// Patent No. 5604201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 92,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-002-202-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4

US-08-021-60BD-22

Sequence 22, Application US/08021608D

Patent No. 5580760

GENERAL INFORMATION:

APPLICANT: LEVENS, DAVID L., DUNCAN,

TITLE OF INVENTION: NOVEL FUSE BINDING

TITLE OF INVENTION: PROTEIN AND CDNA THEREFOR

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: USAC
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERPERCT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,608D
FILING DATE: Z2-FEB-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: TS-FEB-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: A15
FILING DATE: CLASSIFICATION:
NAME: WILLIAM S. FEILER
REGISTRATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
TELEFRANCE/DOCKET NUMBER: 26,728
TELEFRANCE/OPCKET NUMBER: 2026-4063
TELEFRANCE (212) 758-4800
TELEFRAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Mutant 6
US-08-021-608D-22
REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION
TELEBHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                               Query Match 100.
Best Local Similarity 100.
Matches 4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
STRANDEDNESS: Single
TOPOLOGY: Unknown
                                                                                                                                                                                                       TOPOLOGY: lineary
; MOLECULE TYPE: peptide
US-08-481-534-15
                                                                                                                                                                                                                                                                                                                                                                                                          1 RIPR 4
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1 RIPR 4
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chang, Conway
APPLICANT: Chang, Conway
APPLICANT: Chen, Joe
APPLICANT: Chen, Joe
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonde LLP
STREET: 1155 Avenue of the Americas
CITY: New York
COUNTRY: USA
ZIP: 10036
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,589A
FILING DATE: 24-JUL-1996
CLASSIFICATION NUMBER: 30,742
RECIERRINGE/DOCKET NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..4;
COTHER INFORMATION: /product= "Beta-turn"
US-08-685-589A-27
                         NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE DOCKET NUMBER: 8067-026-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELER: 66141
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-685-589A-28
; Sequence 28, Application US/08685589A
; Patent No. 5916872
                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDENESS: unknown
TOPOLOGY: No. 5916872 Relevant
MOLECULE TYPE: peptide
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Peptide LOCATION: 1..4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 3; Conserv
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US-US-583-583-72.

Sequence 27, Application US/08685589A

Patent No. 5916872

GENERAL INFORMATION:

APPLICANT: Chan, Jie

TILE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD

TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY

NUMBER OF SEQUENCES: 222

CORRESPONDENCE ADDRESS: 222

CORRESPONDENCE ADDRESS:

ADDRESSED: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

STREET: 1155 Avenue of the Americas

CITY: New York

COUNTRY: USA

ZIP: 10036

COMPUTER: READBALE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/685,589A

FILING DATE: 24-UUL-1996

CLASSIFICATION NUMBER: FILING DATE:

APPLICATION NUMBER:

FILING DATE:

FILING DATE:

FILING DATE:

FILING DATE:
                                      COUNTY 1. USA.

ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: PAPPLICATION TO SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,160
FILING DATE: 04-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/21,608
FILING DATE: 22-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEB-1993
CLASSIFICATION 1000 NUMBER: 2026-4063U
FELENCHOLICATION NUMBER: 2026-4063U
TELECHONDE: (212) 758-480
TELEFHONE: (212) 751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
STRANDEDARES: Single
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide/Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Mutant 6
   STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
US-08-685-589A-27
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                                   COUNTRY:
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Sequence 12, Application US/09400208B
| Patent No. 6271011
| GENERAL INFORMATION:
| APPLICANT: Lee, Margie
| APPLICANT: Sanchez, Susan
| APPLICANT: Banchez, Susan
| TITLE OF INVENTION: Compositions and Diagnostic Methods
| TITLE OF INVENTION: TOWNER: US/09/400,208B
| CURRENT FILING DATE: 1999-09-21
| PRIOR APPLICATION NUMBER: US 60/028,876
| PRIOR FILING DATE: 1996-10-15
| NUMBER: OF SEQ ID NOS: 27
| SEQ ID NO 12
| LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:peptide motif
OTHER INFORMATION: in Pasteurella multocida neuraminidase
US-09-400-208B-12
                                                                                                                             Sequence 8, Application US/09400208B
Patent No. 6271011
GENERAL INFORMATION:
APPLICANT: Lec, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Sanchez, Susan
TITLE OF INVENTION: Compositions and Diagnostic Methods
FILE REPERENCE: 77-96B
CURRENT APPLICATION NUMBER: US/09/400,208B
CURRENT APPLICATION NUMBER: US/09/400,208B
CURRENT FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: US 60/028,876
PRIOR PELING DATE: 1997-10-15
PRIOR PELING DATE: 1996-10-16
PRIOR PLING DATE: 1996-10-16
PRIOR PLING DATE: 1996-10-16
PRIOR PLING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 8
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ) OTHER INFORMATION: Description of Artificial Sequence:oligopeptide; OTHER INFORMATION: sequence
US-09-400-208B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 3; Conservative
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US-09-400-208B-12
                                                                                              RESULT 10
US-09-400-208B-8
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                                                                                                                                                                                  76.2%; Score 16; DB 2; Length 4; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 76.2%; Score 16; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 4.1e+05; Matches 3; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONTRY:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,589A

TLING DATE: 24-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/08685589A
Patent No. 5916872
GENERAL INFORMATION:
APPLICANT: Chan, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
                                                                  | NAME/KEY: Peptide
| LOCATION: 1..4
| OTHER INFORMATION: /product= "Beta-turn"
US-08-685-589A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
US-08-685-589A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Pennie & Edmonds LLP
1155 Avenue of the Americas
TOPOLOGY: No. 5916872 Relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDENESS: unknown
TOPOLOGY: No. 5916872 Relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: COFUZZI, Laura M.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAK: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                    Query Match 76.2
Best Local Similarity 100.
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                            1 RIP 3
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                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-685-589A-29
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Gaps

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76.2%; Score 16; DB 4; Length 4; 100.0%; Pred. No. 4.1e+05;
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COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE COMPUTER: IBM 486

COMPUTER: IBM 486

OPERATING SYSTEM: WINDOWS FOR WORKGROUPS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: U5/08/221,582A

FILING DATE: April 1, 1994

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,335

FILING DATE: No. 5505946ember 2, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                             US-09-400-122A-12
; Sequence 12, Application US/09400122A
; Patent No. 6767713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.8
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RIP 3
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US-08-221-582A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | FALENT NO. 6'10/13-
| GENERAL INFORMATION:
| APPLICANT: Lee, Margie
| APPLICANT: Sanchez, Susan
| APPLICANT: Sanchez, Susan
| APPLICANT: Sanchez, Susan
| APPLICANT: Henk, Adam
| TITLE OF INVENTION: Pasteurella Neuraminidase Coding Sequences,
| TITLE OF INVENTION: Compositions and Diagnostic Methods
| TITLE OF INVENTION: Compositions and Diagnostic Methods
| FILE REFERENCE: 77-96A
| CURRENT APPLICATION NUMBER: US 09/921
| PRIOR APPLICATION NUMBER: US 60/028,876
| PRIOR APPLICATION NUMBER: US 60/028,482
| PRIOR PELING DATE: 1996-10-16
| PRIOR FILING DATE: 1996-10-15
| NUMBER OF SEQ ID NOS: 27
| SEQ ID NOS: 27
| SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Description of Artificial Sequence:oligopeptide; CTHER INFORMATION: Sequence
US-09-400-122A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                 76.2%; Score 16; DB 3; Length 4; 100.0%; Pred. No. 4.1e+05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76.2%; Score 16; DB 4; Length 4; 100.0%; Pred. No. 4.1e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 4;
                                                                                                                                                                                                                                   Sequence 88 Application US/09417608A

Sequence 88 Application US/09417608A

GENERAL INFORMATION:

APPLICANT: Olsen, Arne

APPLICANT: Ernst, Steffen

TITLE OF INVENTION: Low Allergenic Protein Variants

FILE REFERENCE: 56.200-US

CURRENT APPLICATION NUMBER: US/09/417,608A

CURRENT FILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 101

SEQ ID NO 88

SEQ ID NO 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 4; I
Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/09400122A
Patent No. 6767713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Synthetic
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.2
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial
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US-09-400-122A-8
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lee, Margie
APPLICANT: Sanchez, Susan
APPLICANT: Sanchez, Susan
APPLICANT: Sanchez, Susan
TITLE OF INVENTION: Compositions and Diagnostic Methods
TITLE OF INVENTION: Compositions and Diagnostic Methods
TITLE OF INVENTION: Compositions and Diagnostic Methods
TITLE OF INVENTION: Description and Diagnostic Methods
TITLE OF INVENTION WHERE: US/09/400,122A
CURRENT APPLICATION NUMBER: US 08/951,984
PRIOR PILING DATE: 1996-09-21
PRIOR PLILNG DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-16
PRIOR FILING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 12
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:peptide motif OTHER INFORMATION: in Pasteurella multocida neuraminidase
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Search completed: June 20, 2005, 16:35:39 Job time: 31 secs

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Sequence:

Scoring table:

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Minimum DB Maximum DB

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Title: Perfect score:

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Sequence 6, Appli
Sequence 11, Appl
Sequence 12, Appl
Sequence 131, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
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Sequence 13, Appl
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Sequence 6, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 6, Appl
Sequence 6, Appl
Sequence 10, Appl
Sequence 2, Appl
               | US-10-021-963-7
| US-10-021-963-7
| US-10-021-963-130
| US-10-601-953-1130
| US-10-601-953-1130
| US-10-601-953-1130
| US-10-601-953-1130
| US-10-611-913-1130
| US-10-611-913-1130
| US-10-956-425-14
| US-10-913-861-123
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| US-10-913-961-123
| US-10-913-961-123
| US-10-913-961-123
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| US-10-913-961-130
| US-10-913-913-910-961-961-90
| US-10-913-913-910-90
| US-10-913-910-90
| US-10-910-910-90
| US-10-910-910-9
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-09-955-639C-2
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NS06_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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21: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
22: /cgn2_6/ptodata/2/pubpaa/US108_PUBCOMB.pep:*
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-400-122-8
US-10-462-452-4
US-10-661-953-4
US-10-312-266-4
US-10-311-858B-3
US-10-730-454-88
US-09-778-885-11
US-09-778-885-11
US-09-933-497B-37
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Maximum Match 1008
Listing first 100 summaries
                                                                          protein search, using sw model
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Sequence Sequence Sequence

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Sequence 4, Application US/10601953
Publication No. US20040077540A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Unnctional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Therapeutic Compounds
FILLE OF INVENTION: UNDER: US/10/601,953
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; Sequence 4, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR PLLING DATE: 2003-06-16
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                             76.2%; Score 16; DB 11; I 100.0%; Pred. No. 1.5e+06; iive 0; Mismatches 0;
                    CURRENT APPLICATION NUMBER: US/09/400,122
CURRENT FILING DATE: 1999-09-21
EARLIER APPLICATION NUMBER: US 08/951,984
EARLIER FILING DATE: 1997-10-15
EARLIER PLING DATE: 1996-10-16
EARLIER PLING DATE: 1996-10-16
EARLIER PLING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTY OF 12.0
SOFTWARE: PATENTY OF 2.0
SEARLIER PLING DATE: 1996-10-15
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PATENTY OF 2.0
                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Conservative
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          FILE REFERENCE: 77-96a
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Best Local Similarity
Matches 3; Conserv
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Best Local Similarity
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Sequence 2, Application US/09865914B

Publication No. US20040127396A1

GENERAL INFORMATION:
TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT

TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES

TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES

TITLE OF INVENTION: OF OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT

TITLE OF INVENTION: US OF FURIN AND FURING DISEASES

CURRENT APPLICATION NUMBER: US 60/213,995

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: CA 2,312,109

PRIOR PILING DATE: 2000-06-23

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin version 3.2

LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (4)..(4)
; OTHER INFORMATION: Met358 to Arg358 variant of reactive site of alphal-antitrypsin
US-09-885-914B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(1) OTHER INFORMATION: Ala355 to Arg355 variant of reactive site of alphal-antitrypsin
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                                           Sequence 8, Appli
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 18, Appl
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Sequence 59, Appl
Sequence 60, Appl
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Sequence 179, App
Sequence 2, Appli
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                                 Sequence
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; Bublication No. US20040072153A1
; Publication No. US20040072153A1
; APPLICANT: Lee, Margie
; APPLICANT: Sanchez, Susan
; APPLICANT: Hark, Adam
; TITLE OF INVENTION: Compositions and Diagnostic Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 4;
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100.0%; Pred. No. 1.5e+06;
tive 0; Mismatches 0;
US-09-955-639C-4
US-09-955-639C-8
US-09-955-639C-8
US-09-955-639C-12
US-09-955-639C-13
US-09-955-639C-14
US-09-955-639C-14
US-09-955-639C-15
US-09-955-639C-15
US-09-955-639C-19
US-09-955-639C-19
US-09-955-639C-19
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                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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Best Local Similarity 100.
Matches 4; Conservative
                                                    NAME/KEY: MUTAGEN LOCATION: (1)..(1)
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LOCATION: (4)..(4)
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            TYPE: PRT
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Sequence 11, Application US/10311858B

Sequence 11, Application US/10311858B

Publication No. US20040116656A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application
TITLE OF INVENTION OF SEQ 10 NO 11

LENGTH: 4

LENGTH: 4
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                      76.2%; Score 16; DB 16; Length 4; 100.0%; Pred. No. 1.5e+06; ive 0; Mismatches 0; Indels
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Pred. No. 1.5e+06;
0; Mismatches 1; Indels
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Publication No. US20040175757A1
GRUREAL INFORMATION:
APPLICANT: Olsen, Arne
APPLICANT: Roggen, Erwin
TILE OF INVENTION: Low Allergenic Protein Variants
FILE REPRENCE: 5676.200-US
CURRENT APPLICATION NUMBER: US/10/730,454
CURRENT FILING DATE: 2003-12-08
PRIOR FILING DATE: 1999-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76.2%; Score 16; DB 16; I
100.0%; Pred. No. 1.5e+06;
iive 0; Mismatches 0;
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; OTHER INFORMATION: Peptide Fragments
US-10-311-858B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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SOFTWARE: Patentin version 3.2
SEQ ID NO 88
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Best Local Similarity 75.0%;
Matches 3; Conservative
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                                                                   3; Conservative
                      Query Match
Best Local Similarity
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Best Local Similarity
Matches 3; Conserva
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TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
TITLE OF INVENTION: YY And Methods For Treating And Preventing Obesity
FILE REPERENCE: NPC10567
CURRENT APPLICATION NUMBER: US/10/322,266
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 797
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10311858B

Publication No. US20040116656A1

Fubblication No. US20040116656A1

FUBBRAL INFORMATION:

APPLICANT: SHEN, Jinhuan

TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application

TITLE OF INVENTION: A Kind of Memory-enhancing Peptides and Their Application

CURRENT APPLICATION NUMBER: US/10/311,858B

CURRENT FILING DATE: 2003-08-25

FRIOR APPLICATION NUMBER: PCT/CN01/00875

FRIOR FILING DATE: 2001-05-28

NUMBER OF SEQ ID NOS: 16

SEQ ID NOS: 16
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1.5e+06;
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                                                                                                                                                                                                                                                                                 76.2%; Score 16; DB 15; L
100.0%; Pred. No. 1.5e+06;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.2%; Score 16; DB 100.0%; Pred. No. 1.5 tive 0; Mismatches
                                                                                                                                                                                                            ; OTHER INFORMATION: Synthetic construct US-10-601-953-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Synthetic construct US-10-322-266-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
; OTHER INFORMATION: Peptide Fragments
US-10-311-858B-3
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/10322266 Publication No. US20040115135A1 GENERAL INFORMATION:
                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                 Query Match 76.2
Best Local Similarity 100.
Matches 3; Conservative
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US-10-311-858B-3
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US-10-322-266-4
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                                                                                                                                                                                                   FEATURE:
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Length 4;

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71.4%; Score 15; DB 9; I
66.7%; Pred. No. 1.5e+06;
tive 1; Mismatches 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 2; Conservative
    Query Match 71.4
Best Local Similarity 66.7
Matches 2, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
CORGANISM: Mus musculus
US-09-933-497B-37
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US-10-021-963-7
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                                                                                                                                                                                                                                                          APPLICANT: Rumar, A. A.
APPLICANT: Rittenhouse, H.G.
APPLICANT: Rittenhouse, H.G.
APPLICANT: Wolfert, R.L.
TUTLE OF INVENTION: Method for detection of metastatic prostate cancer;
FILE REFERENCE: 545.0054031
CURRENT APPLICATION NUMBER: US/10/745,733
CURRENT FILING DATE: 1996-11-14
PRIOR APPLICATION NUMBER: US/08/759,354
PRIOR PILING DATE: 1996-05-02
PRIOR APPLICATION NUMBER: US 08/622,046
PRIOR PELING DATE: 1996-03-26
PRIOR PELING DATE: 1996-05-02
PRIOR PELING DATE: 1999-05-02
PRIOR PELING DATE: 1999-07-22
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FREESEQ FOR WINDOWS VERBION 4.0
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US-09-778-885-11

SQUENCE 11, Application US/09778885

Publication No. US2002039748A1

GENERAL INFORMATION:

APPLICANT: Contain Donald C.

APPLICANT: Gao, Zeren

TITLE OF INVENTION: KUNITZ DOMAIN POLYEPTIDE AND MATERIALS

TITLE OF INVENTION: AND METHODS FOR MAKING IT

FILE REPERENCE: 98-22

CURRENT APPLICATION NUMBER: US/09/778,885

CURRENT PILING DATE: 1999-05-26

PRIOR PILING DATE: 1999-05-26

PRIOR PILING DATE: 1999-05-26

PRIOR PILING DATE: 1998-05-26

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
71.4%; Score 15; DB 16; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.5e+06;
Matches 2; Conservative 1; Mismatches 0; Indels
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                                          Sequence 43, Application US/10745733
Publication No. US20040259113A1
GENERAL INPORMATION:
APPLICANT: Tindall, D.J.
APPLICANT: Young, C.Y.F.
APPLICANT: Kilee, G.G.
APPLICANT: Saedi, M.S.
APPLICANT: Saedi, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
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; ORGANISM: Homo sapiens
US-10-745-733-43
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1 RVP 3
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                                                                                                                                                                                             Sequence 37, Application US/09933497B

Patent No. US20020098193A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGLOBIN-LIKE DOMAINS WITH INCREASED HALF LIVES
FILE REFERENCE: UTSD:483

CURRENT FAPLICATION NUMBER: US/09/933,497B

CURRENT FILING DATE: 1996-03-07

PRIOR PILING DATE: 1996-03-18

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver: 2.1

SEQ ID NOS: 37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 15; DB 9; Length 4; Pred. No. 1.5e+06; 1; Mismatches 0; Indels
0; Indels
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Sequence 6, Application US/09819136

Patent No. US20020146789A1

GENERAL INFORMATION:

APPLICANT: Conklin, Darrell C.

APPLICANT: GAO, Zeren

TILLE OF INVENTION: MULTI-DOMAIN PROTEINASE INHIBITOR

FILE REFERENCE: 00-25

CURRENT APPLICATION NUMBER: US/09/819,136

CURRENT APPLICATION NUMBER: US 60/193,642

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PastSEQ for Windows Version 3.0

SEQ ID NO 6

LENGTH: 4
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; OTHER INFORMATION: thrombin cleavage site
US-09-819-136-6
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Search completed: June 20, 2005, 16:51:36 Job time : 105 secs
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Publication No. US20040040053A1

GRARRAL INFORMATION:

APPLICANT: No. US20040040053Alura, No. US20040040053Aluo

APPLICANT: Goshima, Naoki

APPLICANT: Kisu, Yasucomo

APPLICANT: Kisu, Yasucomo

APPLICANT: Kisu, Method For the Preparation of Nucleic Acids

FILE REFERENCE: 0942.5600000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Outpy, Steven
APPLICANT: El Shafy, Mohammed Abd
APPLICANT: El Shafy, Mohammed Abd
APPLICANT: El Shafy, Mohammed Abd
APPLICANT: El Shafy, Malini
APPLICANT: de Meireles, Jorge
TITLE OF INVENTION: Compositions and Methods for Enhanced
TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
FILE REFERENT 82-0208:
CURRENT APPLICATION NUMBER: US/10/462,452
CURRENT PILING DATE: 2003-06-16
PRIOR PELICATION NUMBER: 60/393,066
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 790
SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71.4%; Score 15; DB 13; Length 4; 66.7%; Pred. No. 1.5e+06; tive 1; Mismatches 0; Indels
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                                                               APPLICANT: CONKIN, Darrell C.
TITLE OF INVENTION: KUNITZ DOMAIN POLYPEPTIDE ZKUNG
FILE REFERENCE: 98-40
CURRENT PAPLICATION NUMBER: US/10/021,963
CURRENT FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US/09/388,183
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 7
SOPTWARE FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                           ; PEATURE:
; OTHER INFORMATION: Thrombin cleavage site
US-10-021-963-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 130, Application US/10462452; Publication No. US20040037809A1; GENERAL INFORMATION:
Sequence 7, Application US/10021963 Publication No. US20020110887A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.4
Best Local Similarity 66.7
Matches 2; Conservative
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CRGANISM: Homo sapiens
US-10-462-452-130
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2 VPR 4
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RVP 4
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US-10-462-452-130
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Pred. No. 1.5e+06;
1; Mismatches 0;
CURRENT APPLICATION NUMBER: US/10/301,849A
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: JP2001-357821
PRIOR FILING DATE: 2001-11-22
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin version 3.1
LENGTH: 4
                                                                                                                                                  TYPE: PRT ORGANISM: Unknown FEATURE: ORGANISM: Unknown OTHER INFORMATION: Thrombin cleavage site US-10-301-849A-14
                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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2 VPR 4
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Appl Appl Appl Appl Appl Appl Appli Appli

Sequence 29, Sequence 20, Sequence 8,

Sequence 3 Sequence 5

Sequence 28, Sequence 29, Sequence 27, Sequence 28,

1 RIPR 4

Perfect score:

Sequence:

OM protein -

ü : Run Scoring table:

Searched:

seq length: 0 seq length: 4

Minimum DB E Maximum DB E

Database

Sequence 27,

Sequence 28

Sequence 2, 1 Sequence 4, Al Sequence 4, Al Sequence 27, 1

Description

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US-09-372-003-15
US-09-85-918-2
US-09-885-918-2
PCT-US03-19261-4
PCT-US03-19261-4
PCT-US03-19261-4
PCT-US03-19261-4
PCT-US03-19261-4
PCT-US97-12974A-29
US-09-39-0-034C-3
US-09-39-09-39-3
US-09-39-38-38-3
US-09-39-38-38-3
US-09-39-38-38-3
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Query
Match I
                            Score
            Result
No.
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Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                6959266 seqs, 1168006243 residues
                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                              US-09-885-914B-2
21
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Sequence 29, Appl Sequence 11, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 81, Appl Sequence 33, Appl Sequence 13, Appl Sequence 11, Appl Sequence 12, Appl Sequence 12, Appl Sequence 87, Appl Sequence 87, Appl Sequence 87, Appl Sequence 87, Appl Sequence 16, Appl Sequence 6, Appli Sequence 6, Appli

Sequence 14, Appli Sequence 11, Appli Sequence 131, Appli Sequence 130, Appli Sequence 13, Appli Sequence 11, Appli Sequence 11, Appli Sequence 212, Appli Sequence 97, Appli Sequence 12, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli

Sequence 36,

Sequence 20 Sequence 20 Sequence 7,

Sequence Sequence

Sequence

Sequence 4, App Sequence 4, App Sequence 183,

SUMMARIES

Gaps

; 0

Indels

```
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESSE:
ADDRESSE: ADDRESSE: ADDRESS:
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 12 BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 21; DB 17; Best Local Similarity 100.0%; Pred. No. 6.4e+06; Matches 4; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 6.4e+06;
iive 0; Mismatches 0;
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-SEP-1995
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92,448-D
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US-09-172-003-15
is Sequence 15, Application US/09372003
is GENERAL INFORMATION:
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TELECOMUNINICATION INFORMATION
TELEPHONE: 312-913-0001
TELEPAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                               TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Noonan, Kevin E REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX:
INFORMATION FOR SEQ ID NO:
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                          TELEFAX: 312-913-0002
                                                                                                                                                                                                      , MOLECULE TYPE: peptide US-09-372-003-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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     TELEPHONE:
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                                                                                                     Sequence 37, Appl Sequence 58, Appl Sequence 201, Appl Sequence 202, App Sequence 202, App Sequence 203, App Sequence 201, App Sequence 203, App Sequence 203, App Sequence 201, App Sequence 201, App Sequence 201, App Sequence 202, App Sequence 203, App Sequence 20
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Seguence 12, Appl
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Sequence 200,
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Sequence 12,
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Sequence 202,
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Sequence 10, Application US/09372003
GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Nelson, Jay
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
                                                                           Sequence 2
Sequence 3
Sequence 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BAR PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
US-08-233-054-246
US-08-233-054-247
US-08-233-054-249
US-08-233-054-249
US-08-233-054-249
US-08-323-054-249
US-08-428-404-200
US-08-428-404-201
US-08-428-404-201
US-08-428-404-203
US-08-428-404-203
US-08-428-4048-201
US-08-428-4048-201
US-08-428-4048-203
US-08-447-211-201
US-08-447-211-201
US-08-447-211-201
US-08-447-211-201
US-08-447-211-201
US-08-447-714-201
US-08-947-794-201
US-08-947-794-201
US-08-947-794-202
US-08-947-794-202
US-08-947-794-202
US-08-947-794-203
US-08-170-985-13
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US-09-882-781-12
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REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 300
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STATE: II
COUNTRY:
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Gaps

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Length 4;

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APPLICANT: Quay, Steven C.

TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
TITLE OF INVENTION: Therapeutic Compounds
FILE REFERENCE: 02-03PCT
CURRENT APPLICATION WUMBER: PCT/US03/19994
CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: 60/392,512
PRIOR APPLICATION NUMBER: 60/392,512
NUMBER OF SEQ ID NOS: 900
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
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6.4e+06;
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ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US97/12974A

FTIING DATE: 23 Jul 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 27. Application PC/TUS9712974A
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-026-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.2%; Score 16; Best Local Similarity 100.0%; Pred. No. Matches 3; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Pennie & Edmonds LLP
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , OTHER INFORMATION: Synthetic construct
PCT-US03-19994-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/685,589
FILING DATE: 24-UL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                              Sequence 4, Application PC/TUS0319994 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212-869-9741
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CITY: New York
STATE: New York
COUNTRY: USA
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                                                                                                     RESULT 5
PCT-US03-19994-4
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                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DUBOIS, Claire
TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
FILE REFERENCE: 85761-28
CURRENT APPLICATION NUMBER: US 60/213,995
PRIOR PELLING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: US 60/213,995
PRIOR PILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-26
PRIOR FILING DATE: 2000-06-23
NUMBER: OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MUTAGEN
LOCATION: (1)...(1)
OTHER INFORMATION: Ala355 to Arg355 variant of reactive site of alphal-antitrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (4)...(4)
; OTHER INFORMATION: Met358 to Arg358 variant of reactive site of alphal-antitrypsin
US-09-885-914B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PEATURE:
OTHER INFORMATION: Variant of Homo sapiens alphal-antitrypsin reactive site
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APPLICANT: B1 Shafy, Mohammed Abd
APPLICANT: Gupta, Malhin
APPLICANT: Gupta, Malhin
APPLICANT: Gupta, Malhin
APPLICANT: General Malhin
APPLICANT: General Malhin
APPLICANT: General Malhin
TITLE OF INVENTION: Mucosal-Delivery of Interferon Beta
FILE REFERENCE: 02-02-CT
CURRENT APPLICATION NUMBER: PCT/US03/19261
CURRENT FILING DATE: 2003-06-18
PRIOR PPLICATION NUMBER: 60/393,066
PRIOR PILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 790
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4;
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GENERAL INFORMATION:
APPLICANT: Quay, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 3; Conservative
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Best Local Similarity 100.
Matches 4; Conservative
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1 RIPR 4
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RIPR
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PCT-US03-19261-4
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Best Local Similarity
                       Matches
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GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chang, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
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ZIP: 1036

ZIP: 1036

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OMPUTER: IBM PC COMPATIBLE
OMPRATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12974A
FILING DATE: 23 Jul 97
CLASSIFICATION:
PRIOR APPLICATION WHERE: US 08/685,589
FILING DATE: 24-JUL-1996
ATTOMENYAGENT INFORMATION:
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LOCATION: 1..4
OTHER INFORMATION: /product= "Beta-turn"
                                                                                                                                                                   NAME/KEY: Peptide

LOCATION: 1..4

CTHER INFORMATION: /product= "Beta-turn"

PCT-US97-12974A-27
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REFERENCE/OCKET NUMBER: 8067-026-228
TELECOMMUTCATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Pennie & Edmonds LLP
1155 Avenue of the Americas
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INFORMATION FOR SEQ ID NO: 28
SEQUENCE CHARACTERISTICS:
INPORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: unknown
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATHRF.
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STRANDEDNESS: unb
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STATE: New York
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PCT-US97-12974A-28
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76.2%; Score 16; DB 1; Length 4;

Query Match

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                                                                                                                                                                                               Sequence 29, Application PC/TUS9712974A
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Chang, Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: SPECTRUM ANTIMICROBIAL ACTIVITY
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/12974A
FILING DATE: 23 Jul 97
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.2%; Score 16; DB 1; Le Best Local Similarity 100.0%; Pred. No. 6.4e+06; Matches 3; Conservative 0; Mismatches 0;
100.0%; Pred. No. 6.4e+06; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , LOCATION: 1..4 , OTHER INFORMATION: /product= "Beta-turn" PCT-US97-12974A-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8067-026-228
                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/685,589
FILING DATE: 24-0U1-1996
ATTORNEY INFORMATION:
NAME: COTUZZI, LANTA A. 1
REGISTRATION NUMBER: 30,742
REFERNICE/DOCKET NUMBER: 8067-026-22
TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT-US97-19557-27
Sequence 27, Application PC/TUS9719557
GENERAL INFORMATION:
APPLICANT: Chang, Conway
APPLICANT: Gu, Leo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 212-869-9741
TELEX: 66141
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SS: unknown
not relevant
                     3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid STRANDEDNESS: un)
                                                               1 RIP 3
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Ela PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19557
FLING DATE: Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: CCTUZZi, LAULTA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 30,742
TELERPHONE: 212-790-9090
TELERPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application PC/TUS9719557
GENERAL INFORMATION:
APPLICANT: Chang Conway
APPLICANT: Gu, Leo
APPLICANT: Chen, Jie
TITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76.2%; Score 16; DB 1; Le
100.0%; Pred. No. 6.4e+06;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: Peptide

1 LOCATION: 1..4

) OTHER INFORMATION: /product= "Beta-turn"

PCT-US97-19557-28
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COTUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-048-228
TELECOMMUNICATION INFORMATION:
TELEFAN: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Pennie & Edmouwe ADDRESSEE: STREET: 1155 Avenue of the Americas CITY: New York STATE: New York COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELERY: 212-00,
TELERY: 66141
INFORMATION FOR SEQ ID NO: 2'
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                         TELEPAX: 212-869-9741
TELEX: 66141
INPORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRAUDEDNESS: unknown
                                                                                                                                                                                                                                                                                                         STRANDEDNESS: unknown
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.2
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SS: unknown
not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RIP 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
PCT-US97-19557-29
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Sequence 28, Application PC/TUS9719557

Sequence 28, Application PC/TUS9719557

Sequence 28, Application PC/TUS9719557

Sequence 28, Application PC/TUS9719557

APPLICANT: Chang, Conway

APPLICANT: Chang, Leo

APPLICANT: Chen, Jis

TITLE OF INVENTION: 24211

CORRESPONDENCES: 2411

CORRESPONDENCES: 2411

CORRESPONDENCES: 2411

CORRESPONDENCES: 2411

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds LLP

STREET: 1155 Avenue of the Americas

CITY: New York

COUNTRY: New York

COUNTRY: USA

ZIP: 10036

CONPUTER READABLE FORM:

MEDIUM TREE: Floppy disk

COMPUTER: IBM PC Compatible

COMPUTER: DATENING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTON DATA:

APPLICATION NUMBER: PCT/US97/19557

FILING DATE: herewith
                                                                                                                                                                                                       ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/19557
FILING DATE: herewith
CLASSIFICATION:
  APPLICANT: Chen, Jie
IITLE OF INVENTION: CYCLIC PEPTIDES HAVING BROAD
NUMBER OF SEQUENCES: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY AGENT INFORMATION:
NAME: COLUZZI, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 8067-048-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFRA: 212-869-9741
TELERA: 66141-869-9741
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: Peptide

LOCATION: 1..4

: OTHER INFORMATION: /product= "Beta-turn"

PCT-US97-19557-27
                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: unknown
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.2
Best Local Similarity 100.
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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Gaps

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ZIP: 80303
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LUPOLOGY: single MOLECULE TYPE: peptide HYPOTHETICAL: NO 8-951-984-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 IPR 4
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                                                                                                                                                                                                                                            RESULT 12
US-07-929-181B-20
i Sequence 20, Application US/07929181B
j GENERAL INFORMATION:
TITLE OF INVENTION: TETRAPEPTIDE AND METHOD OF USE
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHELDON & MAK
STREET: 401 Florence Street, First Floor
CITY: Palo Alto
STATE: COUNTRY: USA
COUNTRY: USA
                                                                              Length 4;
                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USAR
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk, 3.50 inch, 1.44 MB
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/929,181B
FILING DATE: 07-AUG-1992
CLASSIFICATION: 514
ATTORIS/AGENT INFORMATION:
NAME: CTARILIL, RAYMOND B
REGISTRATION NUMBER: 32,845
REGISTRATION NUMBER: 32,845
REGISTRATION NUMBER: AATH-10007.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-533
TELEFAX: 415-322-533
TILLEFAX: 415-322-533
TILLEFAX: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08951984
GENERAL INFORMATION:
APPLICANT: Lee, Margie
APPLICANT: Henk, Adam
TITLE OF INVENTION: Compositions and Methods
TITLE OF SEQUENCES: 11
CORRESPONDENCE 11
CORRESPONDENCE SHOWER ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
                                                                          Query Match 76.2%; Score 16; DB 1; Le Best Local Similarity 100.0%; Pred. No. 6.4e+06; Matches 3; Conservative 0; Mismatches 0;
; LOCATION: 1..4
; OTHER INFORMATION: /product= "Beta-turn"
PCT-US97-19557-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Prec. ...
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Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Boulder
                                                                                                                                                            1 RIP 3
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US-08-951-984-8
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Sequence 3 Application US/09290034C

GENERAL INFORMATION:
APPLICANT: Thomas, Gary
FARDILGANT: Thomas, Gary
TITLE OF INVENTION:
TITLE OF INVENTION: Activity
FILE REPERENCE: 9244e-1
CURRENT APPLICATION NUMBER: US/09/290,034C
CURRENT APPLICATION NUMBER: 60/081,034
FRIOR APPLICATION NUMBER: 60/081,034
FRIOR APPLICATION NUMBER: 60/081,034
FRIOR PRILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 3
LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 76.2%; Score 16; DB 13; Length 4; Best Local Similarity 100.0%; Pred. No. 6.4e+06; Matches 3; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE: 15-OCT-1997

CLASSIFICATION NUMBER: WS 60/028,482

PRICATION NUMBER: WS 60/028,482

PRICATION NUMBER: US 60/028,482

PILING DATE: 15-OCT-1996

PRICATION NUMBER: US 60/028,876

PILING DATE: 16-OCT-1996

ATPLICATION NUMBER: US 60/028,876

FILING DATE: 16-OCT-1996

ATPLICATION NUMBER: 33,878

REFERENCEY/AGENT INFORMATION:

REGISTRATION NUMBER: 33,878

REGISTRATION INFORMATION:

TELEPOMMULICATION INFORMATION:

TELEPRAX: (303) 499-8089

INPORMATION FOR SEQ ID NO: 8:

SEQUENCE CHRARACTERISTICS:

LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 76.2%; Score 16; DB 16; I
Best Local Similarity 100.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 0;
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RESULT 15

US-09-290-034C-5

US-09-290-034C-5

Sequence 5, Application US/09290034C

GENERAL INFORMATION:
APPLICANT: Thomas, Gary

TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
TITLE OF INVENTION: Activity
FILE REFERENCE: 9244-8

CURRENT APPLICATION NUMBER: 00/081,034

PRIOR PILING DATE: 1999-04-08

NUMBER OF SEQ ID NOS: 6

SOUTHARR: PatentIn Ver. 2.1

SEQ ID NO 5

LENGTH: 4

TYPE: PRT

OTHER INFORMATION: Description of Artificial Sequence

PEATURE:
OTHER INFORMATION: Recognition sequence

NAME/KEY: SITE

LUCATION: (2)

COTHER INFORMATION: Xaa residue can be any amino acid
US-09-290-034C-5
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Search completed: June 20, 2005, 16:46:42 Job time : 330.5 secs

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0; Gaps

Query Match
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 0; Mismatches 1; Indels

1 RIPR 4 | | | | 1 RXPR 4

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109, App
136, App
136, App
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137, App
152, App
152, App
137, App
134, App
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134, App
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134, App
1353, App
1553, App
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516, App
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1094, Ap
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1650, Ap
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US-10-524-157-1
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124, App
126, App
28, App
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31, App
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                          20, 2005, 16:30:17; Search time 37 Seconds (Without alignments) 13.327 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-992-402-135
US-10-90-9868-8138-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                  583429 segs, 123271311 residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                                                                       protein search, using sw model
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Perfect score:
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Maximum DB
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Result No.

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; OTHER INFORMATION: Peptide fragment of a Fluorogenic Synthetic Peptide US-10-529-163-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-120
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Sequence 28, Application US/10529163

Sequence 28, Application US/10529163

GENERAL INFORMATION:

TITLE OF INVENTION: Methods for Detecting Endocrine Cancer:

TITLE OF INVENTION: Methods for Detecting Endocrine Cancer:

FILE OF INVENTION: Methods for Detecting Endocrine Cancer:

CURRENT APPLICATION NUMBER: US/10/529,163

CURRENT PILING DATE: 2005-03-24

PRIOR PILING DATE: 2002-09-26

PRIOR PILING DATE: 2002-09-26

NUMBER OF SEQ ID NOS: 31

SOFTWARE: Patentin Version 3.2

SEQ ID NO 28
                                                                                                                                                        APPLICANT: Harris, Jennifer L.
APPLICANT: Banciseaux, Robert
APPLICANT: Damoiseaux, Robert
APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: IRM LLC
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses;
TITLE OF INVENTION: Thereof;
FILE REPERENCE: 021288-000410US
CURRENT FILING DATE: 2004-07-14
FRIOR FILING DATE: 2003-07-14
FRIOR FILING DATE: 2003-07-14
NUMBER: OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.2%; Score 16; DB 6; Length 4; Best Local Similarity 75.0%; Pred. No. 5.4e+05; Matches 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 71.4%; Score 15; DB 6; Length 3; Best Local Similarity 66.7%; Pred. No. 5.4e+05; Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                   US-10-892-402-120; Sequence 120, Application US/10892402; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: artificial
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US-10-529-163-30
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Sequence 1661, Ap
Sequence 1662, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: rhodamine protease substrate library peptide US-10-892-402-144
                                                                                                                                                                          APPLICANT: Damoiseaux, Robert
APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: Winssinger, Nicolas
APPLICANT: Winssinger, Nicolas
APPLICANT: IRM LLC
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 021288-000410US
CURRENT APPLICATION NUMBER: US/10/892,402
CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 60/487,464
PRIOR APPLICATION NUMBER: US 60/487,464
PRIOR APPLICATION NUMBER: US 60/487,464
SPRIOR FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 3.0
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PCT-IL05-00211-1661
PCT-IL05-00211-1662
                                                                                 ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 144, Application US/10892402; GENERAL INFORMATION: APPLICANT: Harris, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative 1
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1 RVPR 4
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US-10-892-402-144
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; OTHER INFORMATION: rhodamine protease substrate library peptide
US-10-892-402-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Damoiseaux, Robert
APPLICANT: Damoiseaux, Robert
APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: Winssinger, Nicolas
APPLICANT: IRM LLC
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 021288-000410US
CURRENT APPLICATION NUMBER: US 60/487,464
FRICH APPLICATION NUMBER: US 60/487,464
FRICH FILING DATE: 2003-07-14
FRICH FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 3.0
       APPLICANT: IRM LLC
TITLE OF INVENTION: Pluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 021288-000410US
CURRENT APPLICATION NUMBER: US/10/892,402
CURRENT APPLICATION NUMBER: US 60/487,464
PRIOR APPLICATION NUMBER: US 60/487,464
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 15; DB 6; Length 4;
Pred. No. 5.4e+05;
1; Mismatches 0; Indels
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APPLICANT: Damoiseaux, Robert
APPLICANT: Backes, Bradley J.
APPLICANT: Winssinger, Nicolas
APPLICANT: IRM LLC
                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7%;
Matches 2; Conservative
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; Sequence 30, Application US/10529163
; GENERAL INFORMATION:
; APPLICANT: YOUSEF, et al.
; TITLE OF INVERTION: Methods for Detecting Endocrine Cancer;
; FILE REFERENCE: 11757.82USWO
; CURRENT APPLICATION NUMBER: US 60/414,107
; PRIOR APPLICATION NUMBER: US 60/414,107
; PRIOR FILING DATE: 2002-09-26
; PRIOR FILING DATE: 2002-09-26
; RIOR APPLICATION NUMBER: US 60/450,406
; RIOR PRIOR DATE: 2003-02-26
; ROW FILING DATE: 2003-02-26
; ROW FILING DATE: 2003-03-25
; SEQ ID NOS: 31
; SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Backes, Jennifer L.
APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: Winssinger, Nicolas
APPLICANT: Winssinger, Nicolas
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
FILE REPERENCE: 021288-0004100S
CURRENT FILING DATE: 2004-07-14
FRIOR PRICATION NUMBER: US 60/487,464
PRIOR FILING DATE: 2003-07-14
FRIOR FILING DATE: 2003-07-14
SOFTWARE PASTES OF FOR WINDOWS VERSION 3.0
SEQ ID NO: 11
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.4%; Score 15; DB 6; Length 3; Best Local Similarity 66.7%; Pred. No. 5.4e+05; Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.4%; Score 15; DB 6; Length 4; Best Local Similarity 66.7%; Pred. No. 5.4e+05; Matches 2; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Peptide Portion of Trypsin Substrate US-10-529-163-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
US-10-892-402-11
; Sequence 11, Application US/10892402
; GENERAL INFORMATION:
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; Sequence 59, Application US/10892402
; GENERAL INFORMATION:
; APPLICANT: Harris, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Damoiseaux, Robert
Backes, Bradley J.
Winssinger, Nicolas
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial
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1 VPR 3
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TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
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Best Local Similarity
Matches 2; Conserv
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1 LPR 3
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GENERAL INFORMATION:

APPLICANT: Byrd, Devon

APPLICANT: Youg, Alice

APPLICANT: Toug, Alice

APPLICANT: Woug, Alice

TITLE OF INVENTION: Compositions and Methods for Molecular Biology

TITLE OF INVENTION: Compositions and Methods for Molecular Biology

TITLE OF INVENTION: Compositions and Methods for Molecular Biology

CURRENT APPLICATION NUMBER: US/11/106,715

CURRENT PILING DATE: 2005-04-15

PRIOR PEPLICATION NUMBER: US 60/400,704

PRIOR APPLICATION NUMBER: US 60/403,095

PRIOR APPLICATION NUMBER: US 60/403,095
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US-10-123-036B-17
Sequence 17, Application US/10123036B
Sequence 17, Application US/10123036B
GENERAL INFORMATION:
APPLICATURE OF INVENTION: METHODS FOR THE TREATMENT OF HEPATIC DISORDERS
FILE REFERENCE: 0010872/0483963
CURRENT APPLICATION NUMBER: US/10/123,036B
CURRENT PILING DATE: 2002-04-15
PRIOR FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.3
SEQ ID NOS: 18
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1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                 71.4%; Score 15; DB 6; Length 4; 66.7%; Pred. No. 5.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                CURRENT APPLICATION NUMBER: US/10/892,402
CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 60/487,464
PRIOR FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 104
FILE REFERENCE: 021288-000410US
                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 66.7
Matches 2; Conservative
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Matches 2; Conservative
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ORGANISM: Homo sapiens
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1 RVP 3
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2 VPR 4
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US-11-106-715-87
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; OTHER INFORMATION: rhodamine protease substrate library peptide US-10-892-402-76
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL BEACKES, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: MINSSINGET, Nicolas
APPLICANT: IRM LiAC
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses;
TITLE OF INVENTION: Pluorogenic Enzyme Substrates and Uses;
TITLE OF INVENTION: Pleaced.
FILE REFERENCE: 021288-000410US
CURRENT FILING DATE: 2004-07-14
RRIOR APPLICATION NUMBER: US 60/487,464
FRIOR FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FEBELSEQ for Windows Version 3.0
SEQ ID NO 80
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Harrie, Jennifer L.
APPLICANT: Damoiseaux, Robert
APPLICANT: Damoiseaux, Robert
APPLICANT: Backes, Bradley J.
APPLICANT: Winssinger, Nicolas
APPLICANT: IRM LLC
TITLE OF INVENTION: Fluorogenic Bnzyme Substrates and Uses;
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: WIMBER: US/10/892,402
CURRENT APPLICATION NUMBER: US 60/487,464
FRIOR PILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                             71.4%; Score 15; DB 7; Length 4; 66.7%; Pred. No. 5.4e+05; ive 1; Mismatches 0; Indels
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: thrombin cleavage site
US-11-106-715-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 76, Application US/10892402 GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7
Matches 2; Conservative
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; OTHER INFORMATION: rhodamine protease substrate library peptide US-10-892-402-80
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                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barris, Jennifer L.
APPLICANT: Damoiseaux, Robert
APPLICANT: Damoiseaux, Robert
APPLICANT: Backes, Bradley J.
APPLICANT: Winssinger, Nicolas
APPLICANT: IRM LLC
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereoff
FILE REFERENCE: 021288-000410US
CURRENT APPLICATION NUMBER: US 60/407-14
PRIOR APPLICATION NUMBER: US 60/487,464
PRIOR FILING DATE: 2003-07-14
NUMBER OF SEQ ID NOS: 155
SOFTURE OF SEQ ID NOS: 155
SED ID NO 84
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APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: Hinssinger, Nicolas
APPLICANT: TRM LLC.
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
FILE REPERSING: 021288-000410US
CURRENT PLILING DATE: 2004-07-14
PRIOR FILING DATE: 2005-07-14
PRIOR FILING DATE: 2005-07-14
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                         Score 14; DB 6; Length 4; Pred. No. 5.4e+05; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                  RESULT 14
US-10-892-402-84
Sequence 84, Application US/10892402
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
                                                                           Query Match
Best Local Similarity 66.7%;
Matches 2; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 66.7
Matches 2; Conservative
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US-10-892-402-132
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                           1; Indels
   Length 4;
Score 14; DB 6; I
Pred. No. 5.4e+05;
0; Mismatches 1;
 Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
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Search completed: June 20, 2005, 16:48:01 Job time : 38 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

- protein search, using sw model OM protein June 20, 2005, 16:01:11; Search time 23 Seconds (without alignments) 16.733 Million cell updates/sec Run on:

US-09-885-914B-3 19 1 RVKR 4 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

98

seq length: 0 seq length: 4 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote T-cell receptor be R-phycoerythrin al bradykinin-potenti - Cer phospholipase C (E endoglucanase F phagocytosis-stimu hypothetical prote hypothetical prote myosin-light-chain protamine P1 - ora synaptosomal-assoc FMRFamide - polych T-cell receptor be cardioexcitatory n angiotensin-conver histidinol dehydro bradykinin-potenti growth-modulating bursin - chicken bursin - chicken antho-RFamide neur neuropeptide Antho autho-RF amide neu carbon-monoxide de ubiquitin - rat protamine P1 - (Ы Description protamine FMRFamide SUMMARIES 140870 140804 PQ0010 S13894 T146627 T146627 AP27565 B37196 F37196 GKHU ECXAA A02147 D41654 D41654 A25844 S39390 161883 E44823 E44823 I37013 I18439 PL0146 A35779 160418 DB Query Match Length Score Result No.

ninerheli.	aupernericar	cell Burrace adnes	glucan 1,4-alpha-g	hypothetical prote	schwannomin - mous	branched-chain-ami	alobulin IV alpha	ribosomal protein	D-mannonate hydrol	Ig heavy chain CRD	T-cell receptor be	T-cell receptor be	T-cell receptor be	gamma subunit of P	COI intron 16 prot	thyroliberin - she	thyroliberin - eas	thyroliberin - Bom	TRH-like tripeptid	gene p20K protein	T-cell receptor be	tyrogine protein k	cytochrome-c oxida	cnyroliberin - pig	Spinar Cord peptia	thurstronin-releas	thyroglobulin - do	profess D - Bacher	hypothetical prote	metallothionein-A	Ig heavy chain CRD	T-cell receptor be	protein-glutamine	pallidipin - assas	carbon-monoxide de	T-cell receptor be	T-cell receptor be	Tyrosine-meranocyc	T-cell receptor be	T-cell receptor be	blood cell protein	starvation-induced	RPCH-related neuro	Ig mu chain V regi	T-cell receptor be	biotin A - Citroba	achatin-I - giant	T-cell receptor be	-cell recep	-cell recep	-cell recep	-cell recep	cell rece	-cell recep	dasar rest	
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ALIGNMENTS

RESULT 1

phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)
C;Species: Clostridium perfringens
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000
C;Accession: 140870
R;Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.
Microbiol. Immunol. 36, 603-613, 1992
A;Title: Role of the upstream region containing an intrinsic DNA curvature in the negativ
A;Reference number: I40870; MUID:92396045; PMID:1522810

phenol 2-monooxyge

Gaps

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C;Accession: T46627
R;Chang, S.; Puryea, J.; Funkhouser, E.A.; Newton, R.J.; Cairney, J.
submitted to the EMBL Data Library, July 1995
A;Description: Cloning of a chitinase homolog which lacks chitin binding sites and is dow A;Reference number: Z23105
A;Accession: T46627
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J. Exp. Med. 114, 115-124, 1991
A;Tile: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
histidinol dehydrogenase (EC 1.1.1.23) - wild cabbage (fragment)
C;Species: Brassica oleracea (wild cabbage)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: S13894
R;Magai, A.; Scheidegger, A.
Arch. Biochem. Biophys. 284, 127-132, 1991
A;Title: Purification and characterization of histidinol dehydrogenase from cabbage.
A;Title: Durification and characterization of histidinol dehydrogenase from cabbage.
A;Reference number: S13894; MUID:91112783; PMID:1988490
A;Residues: 13 4865
C;Keywords: dimer; NAD; oxidoreductase
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A,Residues: 1-4 <PEE>
A,FCross-references: UNIPROT:Q8JZN5; UNIPROT:P54729; UNIPROT:Q8CBY1; UNIPROT:Q8CCCO
A,FCross-references: UNIPROT:Q8JZN5; UNIPROT:Q8CBY1; UNIPROT:Q8CCCCO
A,FEXperimental source: newborn thymus, strain BALB/c
C,Keywords: T-cell receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein c4 - loblolly pine
C;Species: Pinus taeda (loblolly pine)
C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell receptor beta chain V-D-J region (140-2K) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: PT0721
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A;Experimental source: strain s6PT2xs6PT3; 8 month seedlings
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Accession: PT0721
A;Status: translation not shown
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Best Local Similarity
Matches 1; Conserv
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2 MK 3
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R;Mishra, S.; Beguin, P.; Aubert, J.
J. Bacteriol. 173, 80-85, 199
A;Title: Transcription of clostridium thermoncellum endoglucanase genes celF and celD.
A;Reference number: 140804; MUID:91100322; PMID:1987137
A;Accession: 140804
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-4 <RES>
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PQ0010
Note that the parting enzyme inhibitor (FLP-3) - common fig
NyAlternate names: ficus latex peptide 3
Cyspecies: Picus carica (common fig)
Cybecies: Picus carica (common fig)
Cybecies: Poun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
CyAccession: PQ0010
CyAccession: PQ0010
CyAccession: SQ0010
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C;Species: Clostridium thermocellum
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40804
                                                                                                                                                                              A;Cross-references: EMBL:X62825; NID:g40622; PIDN:CAA44636.1; PID:g4377417 C;Genetics: A;Gene: plc C;Keywords: plc C;Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.9%; Score 11; DB 2; Length 4; 66.7%; Pred. No. 2.8e+05;
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C;Genetics:
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A;Residues: 1-3 <MAR>
A;Experimental source: latex
C;Keywords: angiotensin-converting enzyme inhibitor
                                A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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Best Local Similarity 66.7.
Best Local 2; Conservative
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Matches 1; Conservative
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A; Accession: PQ0010
                                                                                                                                             A; Residues: 1-4 < RES>
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1 MKR 3
                                                                                       A; Molecule type: DNA
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1 MKK 3
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C;Species: Gallus gallus (chicken)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C;Accession: A60898
R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.
Science 21, 997-999, 1986
A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the A;Reference number: A60898; MUID:86122916; PMID:3484838
A;Accession: A60898
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C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A2666
R;Grimmelikhuijzen, C.J.P.; Graff, D.
Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986
A;Title: Isolation of <Glu-Gly-Arg-Phe-NH2 (Antho-RFamide), a neuropeptide from sea anemc A;Reference number: A2666; MUID:87092339; PMID:2879288
A;Accession: A2666
A;Accession: A2666
A;Accession: A2666
A;Accession: A2666
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A/Cross-references: UNIPROT:P10419
C;Comment: The function of this peptide is not known but it could act as a transmitter at C;Comment: Synthetic and natural peptides had identical properties.
C;Superfamily: RFamide neuropeptide
C;Superfamily: RFamide neuropeptide
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
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                                                                                                                                                                                                                                                                              C;Accession: A01421
R;Schlesinger, D.H.; Pickart, L.; Thaler, M.M.
Experientia 33, 324-325, 1977
A;Title: Growth-modulating serum tripeptide is glycyl-histidyl-lysine.
A;Reference number: A01421; MUID:77162369; PMID:858356
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A;Residues: 1-3 «AUD»
C;Keywords: amidated carboxyl end; hormone
F;3/Modified site: amidated carboxyl end (Gly) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 1-3 <SCH>
A;Note: this serum tripeptide is found to stimulate growth of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 26.3%; Score 5; DB 3; Length 3; Similarity 100.0%; Pred. No. 2.8e+05; 1; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                       - human
                                                                                                                                                                                                       growth-modulating peptide
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Matches 1; Conserva
                                                    2 K 2
3 K 3
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GKHU
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A60898
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C;Species: Bothrops insularis (island jararaca)
C;Species: Bothrops insularis (island jararaca)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 30-Jun-2001
C;Accession: B37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J; Protein Chem. 9, 21-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
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bradykinin-potentiating peptide 6 - island jararaca
C;Species Bothrops insularis (island jararaca)
C;Species Bothrops insularis (island jararaca)
C;Date: 15-Unn-2001 #sequence_revision 15-Unn-2001 #text_change 15-Unn-2001
C;Accession: F37196
R;Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A;Title: Primary structure and biological activity of bradykinin potentiating peptides
A;Reference number: A37196; MUID:90351557; PMID:2386615
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                                                                                                     A22565
R-phycoerythrin alpha-1 chain - red alga (Gastroclonium coulteri) (fragment)
C; Species: Gastroclonium coulteri
C; Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C; Accession: A22565
R; Klotz, A.V.; Glazer, A.N.
J. Biol. Chem. 260, 4856-4863, 1985
A; Mitle: Characterization of the bilin attachment sites in R-phycoerythrin. A; Reference number: A22565; MUID:85182601; PMID:3886644
A; Accession: A22565
A; Molecule type: protein
A; Residues: 1-3 «KLO»
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A;Mesidues: 1-3 <CIN>
C;Kesidues: pyroglutamic acid
P;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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100.0%; Pred. No. 2.8e+05;
iive 0; Mismatches 0; Indels
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A;Molecule type: protein
A;Residues: 1-3 <CIN>
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A; Status: preliminary
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bypothetical protein (sodC 5' region) - Haemophilus parainfluenzae (fragment)
hypothetical protein (sodC 5' region) - Haemophilus parainfluenzae
C;Species: Haemophilus parainfluenzae
C;Date: 12-Um-1992 #sequence_revision 12-Um-1992 #text_change 24-Feb-1995
C;Accession: D41654 #sequence_revision 12-Um-1992 #text_change 24-Feb-1995
C;Accession: D41654 P.R.; Loynds, B.M.
J. Bacteriol. 173, 749-7457, 1991
A;Kroll, J.S.; Langford, P.R.; Loynds, B.M.
J. Bacteriol. 173, 749-7457, 1991
A;Reference number: A41654; MUID:92041655; PMID:1938942
A;Accession: D41654
A;Retain are preliminary
A;Molecule type: DNA
A;Residues: 1-4 <KRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Species: Jankar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A01147
R;Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
B;Ochem Biophys Res. Commun. 47, 172-179, 1972
A;Title: The characteristics, isolation and synthesis of the phagocytosis stimulating pe
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140505
hypothetical protein 3 (4 aa) - Bacillus stearothermophilus
C;Specise: Bacillus stearothermophilus
C;Date: 12-Nug-1996 #sequence_revision 12-Aug-1996 #text_change 15-Oct-1999
C;Accession: 140505
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F;4/Modified site: amidated carboxyl end (Phe) #status experimental
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                                                                                     DB 1; Length 4;
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                                                                                     26.3%; Score 5; DB 1
100.0%; Pred. No. 2.8
tive 0; Mismatches
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R;Waye, M.M.; Winter, G.

Bur. J. Blochem. 158, 505-510, 1986

AyTitle: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA syntly AyItle: A transcription terminator in the 5' non-coding region of the tyrosyl tRNA syntly A; Reference number: 140503, MUID:86274732; PMID:3525162

A;Accession: 140505

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Molecule type: DNA

A;Molecule type: DNA

A;Rosidues: 1-4 <RES>

A;Cross-references: EMBL:X04193; NID:g40233; PIDN:CAA27783.1; PID:g580944

Query Match

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 K 4

Db 4 K 4

Search completed: June 20, 2005, 16:34:36

Job time: 24 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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protein search, using sw model OM protein Run on:

June 20, 2005, 15:59:16 ; Search time 109.5 Seconds (without alignments) 18.706 Million cell updates/sec

US-09-885-914B-3 19

1 RVKR 4 score: Sequence: Title: Perfect

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

56 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 4 Minimum I Maximum I Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P24272 vibrio fisc	P58706 anthopleura	Q08433 rattus sp.	P01157 homo sapien	-	P42562 hirudo medi	P42563 hirudo medi			P58707 anthopleura		homo	Q96at0 homo sapien	homo	P36515 saccharomyc	P83568 sepia offic		P62971 notophthalm		P62969 ovis aries		P83570 sepia offic	P35904 achatina fu	P58648 octopus min	octop	Q16047 homo sapien
DB ID	1 LUXE VIBFI	1 FYRI ANTEL	2 Q08433	1 GRWM HUMAN	1 DCMS PSECH	1 FAR3 HIRME	1 FAR4 HIRME	1 FFKA ANTEL	1 FLRF HIRME	1 FLRN ANTEL	1 FMRF MACNI	1 TUFT HUMAN	2 Q96AT0	1 EOSI HUMAN	1 YLM1 YEAST	1 ILME_SEPOF	1 THYL_BOMOR	1 THYL NOTVI	1 THYL_PIG	1 THYL SHEEP	1 DCML_PSECH	1 GWA SEPOF	1 ACHI ACHFU	1 OCP1_OCTMI	1 OCP3_OCTMI	2 Q16047
% Query Match Length DB	2.1 3	2.1 4	1.6	5.3	5.3	5.3	5.3	5.3	5.3 4	5.3	26.3 4	26.3 4	5.3	1,1	1.1	5.8 4	5.3 3	5.3 3	5.3	5.3 3	5.3	0.0	0.0	0.0	0.0	0.0
% Query Score Match	8 4.	8 4.	6 3.	2 2	2 5	2	5 2(2 2(5 26	5 26	2	2	2	4 21	4	3	-					0	0	0	0	0
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch). site for the lux operon.";
J. Bacteriol. 172:6797-6802(1990).
-!- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It is a component of the fatty acid reductase complex responsible for converting tetradecanoic acid to the aldehyde which serves as substrate in the luciferase-catalyzed reaction.
-!- CATALYTIC: ATTY TYPT: ATP + an acid + protein = AMP + diphosphate + an acyl-protein thiolester.
-!- PATHWAY: Bioluminescent fatty acid reduction system; second step.
-!- SIMILARITY: Belongs to the luxE family. 01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
05-UTJ-2004 (Rel. 44, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (EC 6.2.1.19) (Acyl-protein synthetase) (Fragment). SEQUENCE FROM N.A.
MEDLINE=9107226; PubMed=2254256;
Swattrana B., Kapoor S., Graham A.F., Meighen B.A.;
I'A new Vibrio fischeri lux gene precedes a bidirectional termination eite for the lux operon."; Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales, Vibrionaceae, Vibrio. NCBI_TaxID=668; SEQUENCE 3 AA; 374 MW; 6AA330300000000 CRC64; 3 A.A. EMBL; M62812; -; NOT_ANNOTATED_CDS. PRT; STANDARD; Ligase; Luminescence Vibrio fischeri. VIBFI LUXE % The state of the

Gaps ö 0; Indels Length 3; Score 8; DB 1; Lo Pred. No. 1.6e+06; 1, Mismatches 42.1%; 50.0%; Conservative Query Match Best Local Similarity

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the unusual, MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z; Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D., Grimmelikhuijzen C.J.P., Grimmelikhuijzen C.J.P., Tisolation of two novel neuropeptides from sea anemones: the unust biologically active L-3-phenyllactyl-Tyr-Arg-Ile-NH2 and its desphenyllactyl fragment Tyr-Arg-Ile-NH2.", Peptides 12:1165-1173(1991). Bukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria; Nynantheae; Actiniidae; Anthopleura. NCBI TaxID=6110; 28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-Antho-Rlamide I [Contains: Antho-Rlamide II].
Anthopleura elegantissima (Sea anemone) 4 AA. PRT; STANDARD; FYRI ANTEL P58706; SEQUENCE RESULT 2 FYRI_ANTEL

ALIGNMENTS

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                       NCBI_TaxID=9606;
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ID _DCMS_P
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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                                          MEDLINE-93391436; PubMed-8397415;
McFarlane I.D., Hudman D., Nothacker H.-P., Grimmelikhuijzen C.J.P.,
"The expansion behaviour of sea anemones may be coordinated by two
inhibitory neuropeptides, Antho-KAamide and Antho-Riamide.";
Proc. R. Soc. Lond., B, Blol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several muscle
groups. May be involved in the expansion phase of feeding
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hown sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=91282758; PubMed=1840486; Sato H., Aono S., Kashiwamata S., Koiwai O.; Sato H., Aono S., Kashiwamata S., Koiwai O.; "Genetic defect of bilirubin UDP-glucuronosyltransferase in the hyperblirubinemic Gunn rat."; Biochem. Biophys. Res. Commun. 177:1161-1164(1991). EMBL, S38636; AAB19259.1; -. GO, GO:0016740; F:transferase activity; IEA.
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1; Mismatches 0; Indels
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Pred. No. 1.6e+06;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Bilirubin UDP-glucuronosyltransferase (Fragment).
                                                                                                                                                                                                           -1- SUBCELLULAR LOCATION: Secreted.
-1- TISSUB SPECIFICITY: Neuron specific.
Amidation; Direct protein sequencing; Neuropeptide.
CHAIN
2 4 Antho-Riamide II.
CHAIN
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                                                                                                                                                                                                                                                                                                                  3-phenyllactic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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-!- CATALYTIC ACTIVITY: CO + H(2)O + A = CO(2) + AH(2).
-!- COFACTOR: Binds 2 2Pe-2S clusters (By similarity).
-!- SUBUNIT: Heterotrimer consisting of a large, a medium and a small
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                                                                                                                       to stimulate
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"Homology and distribution of CO dehydrogenase structural genes in
carboxydotrophic bacteria.";
Arch. Microbiol. 152:335-341(1989).
MEDINE=77162369; PubMed=858356;
Schlesinger D.H., Pickart L., Thaler M.M.;
Schlesinger D.H., Pickart L., Thaler M.M.;
"Growth-modulating serum tripeptide is glycyl-histidyl-lysine.";
Experientia 33:324-325 (1977).
-i- MISCELLANEOUS: This serum tripeptide has been found to stimulat growth of some cell types and to inhibit other types in vitro.
GO, GO:0001558; P:regulation of cell growth; NAS.
Direct protein sequencing.
SEQUENCE 3 AA; 340 MW; 6331E81000000000 CRC64;
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Bradyrhizobiaceae.
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01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Carbon monoxide dehydrogenase small chain (EC 1.2.99.2)
dehydrogenase subunit S) (CO-DH S) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h Similarity 100.0%; Pred. No. 1.6e+06; 1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     26.3%; Score 5; DB 1; Length 3; 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0; Indels
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NON TER 4 4
SEQÜENCE 4 AA; 420 MW; 6DD33DD6F000000 CRC64;
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1996 (Rel. 44, Last annotation update)
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Y WEDLUNE-31391436; PubMed=8397415;

X MEDLUNE-31391436; PubMed=8397415;

A McFarlane I.D., Hudman D., Notacker H.-P., Grimmelikhuijzen C.J.P.;

AT The expansion behaviour of sea anemones may be coordinated by two for inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";

Proc. R. Soc. Lond., B. Biol. Sci. 253:188(1993).

CC Groups. May be involved in the expansion phase of feeding behaviour in sea anemones.

CC Dehaviour in sea anemones.

CC -I- FUNCTION: Inhibits spontaneous contractions in several muscle groups. May be involved in the expansion phase of feeding cc behaviour in sea anemones.

CC -I- TISSUE SPECIFICITY: Neuron specific.

DR PIR; JO1273; JO1273.

KW Amidation; Direct protein sequencing; Neuropeptide.

MOD RES I 1 3-phenyllactic acid.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N; Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; "Identification of RFamide neuropeptides in the medicinal leech.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helisoma trivolvis (Snail).

Bukaryota, Metazoa, Annelida, Clitellata; Hirudinida, Hirudinea, Arhynchobdellida, Hirudiniformes, Hirudinidae; Hirudo.

NCBI_TaxID=6421, 27815;
                                        Nothacker H.-P., Rinehart K.L. Jr., Grimmelikhuijzen C.J.P.; "Isolation of L-3-phenyllactyl-Phe-Lys-Ala-NH2 (Antho-KAamide), novel neuropeptide from sea anemones."; Biochem. Biophys. Res. Commun. 179:1205-1211(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptides 15:31-36(1994).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
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MOD RES 4 4 Phenylalanine amide.
SEQUENCE 4 AA; 582 MW; 69D40729A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             4 4 AA; 512 MW; 6DD339C9A0000000 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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100.0%; Pred. No. 1.6
ive 0; Mismatches
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                          MEDLINE=92028852; PubMed=1681803;
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Similarity 100.0%;
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                                                                                                               MBDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N; Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; Identification of RPamide neuropeptides in the medicinal leech."; Peptides 12:897-908(1991).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bvans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RPamide neuropeptides in the medicinal leech.";
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01-NOV-1995 (Rel. 32, Last sequence update)
05-UUJ-2004 (Rel. 44, Last annotation update)
FMRPanide-like neuropeptide YMRP-amide.
Hirudo medicinalis (Medicinal leech).
Bukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudio.
Hirudo medicinalis (Medicinal leech).
Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
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Anthopleura elegantissima (Sea anemone).
Bukaryota; Metazoa; Chidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides 12:897-908(1991).
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FWRFamide related peptide)
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                                                                                                                                                                                                                                                                                                                      DB 1; Length 4;
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MOD RES 4 4 Phenylalanine amide.
SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
                                                                                                                                                                                                                                             Amidation; Direct protein sequencing; Neuropeptide.
MOD RES 4 4 Phenylalanine amide.
SEQÜENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
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28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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100.0%; Pred. No. 1.6
tive 0; Mismatches
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Best Local Similarity
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IMMUNOGLOBULIN CLASS.
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PIR; A60418; A60418.
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                                   SPECIES=N.virens;
MEDLINE=90259866;
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P01858;
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"Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc.";
Prep. Blochem. 7:261-281(1977).
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-i- MASS SPECIFICITY: NW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
PIR; A35779; A35779.
A36779; A35779; A35779
A36740; Direct protein sequencing; Neuropeptide.
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
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SPECIES=M.nimbosa; TISSUE-Cerebral pedal, and Visceral ganglion;
MEDLINE=77215956; PubMed=877582;
Price D.A., Greenberg M.J.;
"Structure of a molluscan cardioexcitatory neuropeptide.";
Science 197:670-671(1977).
                                                                                                                                                                                                                                      Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
NCBI_TaxID=6110;
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05-JUL-2004 (Rel. 44, Last annotation update)
FMRFamide (Peak C) (Cardioexcitatory neuropeptide)
Macrocallista nimbosm (Sun-ray clam),
Nereis (Sandworm),
Hirudo medicinalis (Medicinal leech), and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26.3%; Score 5; DB 1; Len 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
                                                                                                                                                                                   (Rel. 41, Last sequence update) (Rel. 44, Last annotation update)
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NCBI_TaxID=6594, 6353, 6421, 27815;
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MEDLINE=78012038; PubMed=909875;
                                                                                                                                                                                                                                                                                                                                             SEQUENCE, AND MASS SPECTROMETRY. MEDLINE=90319122; PubMed=1973541;
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Matches 1; Conservative
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SPECIES-H.trivolvis; TISSUE-Kidney;
MEDINTE-94286417; PubMed=791248; DOI=10.1016/0196-9781(94)90166-X;
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.;
"FMRFamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of
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MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;
                        Krajniak K.G., Price D.A., "Authentic FWRFamide is present in the polychaete Nereis virens.";
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-!- SUBCELLUTAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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MOD RES 4 4 Phenylalanine amide.
SEQUENCE 4 AA; 600 MW; 69D40699A0000000 CRC64;
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21-JUL-1986 (Rel. 01, Last sequence update)
25-JUL-2004 (Rel. 44, Last annotation update)
Phagocytosis-știmulating peptide (Tuftsin).
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100.0%; Pred. No. 1.6
vative 0; Mismatches
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Peptides 15:31-36(1994).
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STANDARD;
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Best Local Similarity
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P36515;
   EOSI HUMAN
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YLM1 YEAST
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Both of the colling R., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shovchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Schworthowko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
"Generation and initial analysis of more than 15,000 full-length human
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Tuftsin is essential for maximum stimulation of the phagocytic
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                            26.3%; Score 5; DB 1; Length 4; 100.0%; Pred. No. 1.6e+06; tive 0; Mismatches 0; Indels
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Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC016791; AAH16791.2; -.
SEQUENCE 4 AA; 512 MW; 633DCB56F000000 CRC64;
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Last annotation update)
                                                GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0005809; P:phagocytosis; NAS.
Direct protein sequencing.
SEQUENCE 4 AA; 501 MW; 74176321C000000 CRC64;
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                                                                                                                                                                                                                                                                          Created)
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           activity of neutrophils.
PIR; A02147; A02147.
MIM; 191150; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
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                                                                                                                         Local Similarity 100.
                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                              FLJ30656 protein.
Homo sapiens (Human)
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Q96AT0
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RESULT 14 EOSI_HUMAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 72:4123-4127(1975).

-!- MISCELLANBOUS: These peptides are released from mast cells in lung (and other tissues) during hypersensitivity reactions (anaphylaxis). Their activities, preferentially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of enzymes, and stimutation of the hexose monophosphate shunt. GO; GO:0006935; P:chemotaxis; IDA. GO; GO:0006955; P:immune response; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria."; PEBS Lett. 284:51-56(1991). -- FEBS Lett. 284:51-60 (1991). -- FUNCTION: Putative component of the large subunit of mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                              ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                 Goetzl E.J., Austen K.F.; "Purification and synthesis of eosinophilotactic tetrapeptides of human lung tissue: identification as eosinophil chemotactic factor
                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycoina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.1%; Score 4; DB 1; Length 4; 100.0%; Pred. No. 1.6e+06; ive 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.1%; Score 4; DB 1; Length 4; 100.0%; Pred. No. 1.6e+06; trive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V -> A (in other peptide)
/FTId=VAR_005201.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 AA; 390 MW; 6B05B862A000000 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER 4 4 4 SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Eosinophilotactic peptides.
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                                                                                                                                                                                                                                                                                                                MEDLINE=76078412; PubMed=1060093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct protein sequencing.
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Best Local Similarity
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Search completed: June 20, 2005, 16:33:43 Job time : 109.5 secs

Abul0024 Alpha-MSH Adby559 Protease Adi28884 Human ser Adj57392 Purin inh	Aap20059 Enzyme su Aar37635 Sequence	Aaioosto reprinase Aay44372 Tetrabasi Aab67730 Amino aci	Aau07641 Aillio act Aau07641 Mild-type	Amp52826 HU gp120	Abg31272 Human fac	Ade24598 reast nex Abp98103 Amino aci	Abr40173 Marburg v Adh10700 Strentomy	Add80880 Subtilisi	Aars/630 Sequence Aar48281 Nuclear r	Aare0559 ilesue pi Aare0594 proins.RO	Aars1491 human A-m Aars2965 Human A-m	Aar64811 ScFv-Lys Aar65180 Dibasic a	Pepti	Aaw44279 Human thy	Nucle	Aay82083 HIV 168P Aay82085 HIV enhan	Aab14217 HIV SF162	Aae00920 Cleavage Aab72635 Mammalian	Aab72639 Mammalian Aab62231 PA protei	Aael4288 Thymosin	Abb77181 Human mat	Aae24419 Transport	Adol7055 Peptide a	Abb09213 HIV Env c Aam52115 Anthrax P	PERV typ	Nucie	Abp98107 Amino aci	Endo	Abp71147 Human pro	HIV-1	Rheuma	HIV-1	Exempl	Adglaysi multimeri Adi05537 Novel ade	Adj57388 Peptide f	Adja892s Human pro Adk40309 Antibacte	Adp44091 Human thy	Add30899 Newcastle	Aar37631 Sequence	Aar38742 KEX2 clea bar59927 bloha 1-a	Aar60595 proins KT	2
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5.1.6 Compugen Ltd.		Search time 113.5 Seconds	Aillion cell updates/sec						: 19815											σ.	to the score of the result being printed, of the total score distribution.			Description		Aae35573 Furin cle Adi57391 Furin inh	Aay30777 Peptide u	Aay84215 Amino aci Aab97408 Site-1 pr		Furin	Abp71148 Human pro	Addluss/ Egiin c v Add84924 Tetrapept	Multimer	щ О.	proine	Aau75632 Human myo	Zebra	Furin	Aby 3370 Auman pro Aao30152 Spectrozy	Aae29827 Spectrozy	Ada10588 Spectrory Ada10588 Spectrory	175/
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compu	search, using sw model	20, 2005, 14:16:51; Search t	13.630	-885-914B-3	4.	M62	10.0 , Gapext 0.5	92 seqs, 386760381 residues	hits satisfying chosen parameters:		4	mum Match 0% mum Match 100%	first	Geneseq_16Dec04:*	eneseqp1980s:* eneseqp1990s:*	eneseqp2000s:* eneseqp2001s:*	eneseqp2002s:*	geneseqp2003as:* geneseqp2003bs:*	eneseqp2004s:*	e number of results predicted	reater than or equal to the score of derived by analysis of the total scor	Saidemonis		Length DB ID	Total Co	ਵਾ ਵਾ	4.	44	4.4	4. 4. U TU	4.4	4 4	4.	4. 4 D C	101	4. 4 V	r 4.	y Q		4.4	4 6 ADA10588 4 6 ADA10588 4 6 ADR17421	r
	OM protein - protein	Run on: June		Title: US-09-885-		Scoring table: BLOSUM62	Gapop	Searched: 2105692	Total number of hits	Minimum DB seq length:	ŭ	Post-processing: Minimum Maximum	Listing					6: 9 7: 9		~	score greater t and is derived]			Result Core Query	2006	44	16	10 10	16	16 8	16	16	16	15	112	15	15	15	15	15	24 15 78.9	CT

Aaw25085 Protein C Aay20463 Human mic

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Fusion agent useful for preventing and treating an infectious disease, or a proliferative disease, such as cancer, comprises a transport domain, two cleavage sites, a peptide epitope and a biologically active agent.
                                                                                                                                                       Fusion agent, immunogenic; proliferative disease; infectious disease; cancer; therapy; vaccine; melanoma; Trojan antigen; TA.
                                     ALIGNMENTS
                                                                                                                                                                                                                                                                          (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
AAW25085
         AAY20463
                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 37; 72pp; English.
                                                                                 AAE35573 standard; peptide; 4 AA.
                                                                                                                                    Furin cleavable linker peptide
                                                                                                                                                                                                                                       20-MAY-2002; 2002WO-US015992
                                                                                                                                                                                                                                                         18-MAY-2001; 2001US-0291874P
 0 0
                                                                                                                    17-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                              WPI; 2003-140367/13
63.2
63.2
                                                                                                                                                                                                    WO200294994-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4 AA;
                                                                                                                                                                                   Unidentified
                                                                                                                                                                                                                      28-NOV-2002
12
                                                                                                   AAE35573;
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                                                              RESULT 1
AAE35573
ID AAE3
100
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The invention relates to a fusion agent (Trojan antigen, TA) comprising a transport domain, two cleavage sites, a peptide epitope recognised by an antigen specific receptor on an effector T-lymphocyte precursor cell and a biologically active agent, where there is a cleavage site between the peptide epitope and the biologically active agent and between each biologically active agent. The fusion agent is used to make a cell immunogenic or antigenic. It is also useful for preventing and treating an infectious disease such as viral, bacterial, protozoal, fungal or clear disease, or proliferative disease such as cancer (e.g. melanoma, neural tissue, gastrointestinal, breast, lung, ovarian, testicular, prostate, cervical, bladder, vaginal, liver, renal, bone, haematological or vascular tissue cancer). The invention is used as vaccines. The present sequence is furin cleavable linker peptide. This peptide is used in the exemplification of the invention
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ö Gaps ö Length 4; 0; Indels 100.0%; Score 19; DB 6; I 100.0%; Pred. No. 1.8e+06; iive 0; Mismatches 0; Local Similarity 100. Query Match Matches

ADJ57391 standard; peptide; 4 AA. RVKR 4 RESULT 2 ADJ57391

ADJ57391,

Convertase; inhibitor; furin; antiinflammatory; vulnerary; ophthalmological; dermatorlogical; nephrotropic; hepatotropic; antiinfertility; respiratory-gen.; cardiant; CNS-gen.; cerebroprotective; neuroprotective; noctropic, cytostatic; antiarthritic; (first entry) Furin inhibitor peptide. antiarteriosclerotic. 06-MAY-2004

Unidentified

Location/Qualifiers 'note= "dec-Arg" /note= "Arg-cmk" Key Modified-site Modified-site

WO2004009113-A1

29-JAN-2004

23-JUL-2003; 2003WO-GB003159.

24-JUL-2002; 2002GB-00017136.

(RENO-) RENOVO LTD.

Brunner G; Ferguson MWJ,

WPI; 2004-180270/17.

Use of a convertase inhibitor in the manufacture of a medicament for reducing scarring during the healing of wounds or reducing fibrosis in the treatment of fibrotic conditions.

Example; Page 28; 43pp; English

The present sequence is that of a furin inhibitor peptide. This was used in an example from the invention which showed that furin-like enzymes are involved in platelet-mediated latent transforming growth factor-beta (TGF-beta) activation. The inventors have established that convertase enzymes cutivation of latent transforming growth factor-beta (TGF-beta) in the extracellular space at the site of a wound of a fibrotic conditions.

Thus, the present invention relates to use of convertase inhibitors for the reduction of scarring during the healing of wounds, for reducing fibrosis in the treatment of fibrotic conditions, for reducing fibrosis in the treatment of fibrotic conditions, for reacting wounds to prevent scar formation, for preventing scarring of the eye, nervous fibrotic condition is a fibrotic discate such as glomerulonephritis, cirrhosis of the liver, fibrotic discase, adhesions and restenosis (all fibrotic condition) as a fibrotic discase, adhesions and restenosis (all fibrotic condition) as a fibrotic discase, adhesions and restenosis (all cirrhosis of the liver, fibrocytic discase, adhesions and restenosis (all carring in the pelvis in the region of the fallopian tubes leading to infertility, scarring following injury to the muscles, scarring or scarring in the pelvis in the region of the fallopian tubes leading to serious loss of function, liver fibrosis, pulmonary fibrosis, contaction, central nervous system fibrosis, pulmonary fibrosis, contaction, central nervous system fibrosis following myocardial hiserables. neurodegenerative disorders (e.g. Alzheimer's disease), proliferative vitreoretinopathy, arthritis, arteriosclerosis and cancer.

Sequence 4 AA;

Gaps ; 0 100.0%; Score 19; DB 8; Length 4; 100.0%; Pred. No. 1.8e+06; rive 0; Mismatches 0; Indels 4; Conservative Query Match Best Local Similarity Matches

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/note= "attached to MCA"
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                     Location/Qualifiers
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                                                                                                                                             99WO-US018544
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Best Local Similarity 75.0%;
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                                                                                                                                                                                                                                           ESPENSHADE P J.
                                                                                                                                                                                                                                                         GOLDSTEIN J L.
RAWSON R B.
                                                                                                                                                                                                                                                                                                                                           WPI; 2000-224327/19.
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                                                                                                                                                                                                                   BROWN M S.
CHENG D.
                                   Misc-difference
                                                          Misc-difference
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                                                                                                                                             13-AUG-1999;
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Sakai J;
Synthetic
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(ESPE/)
(GOLD/)
(RAWS/)
                                                                                                                                                                                                       (TEXA)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
SXXXXXXXXXXXXXX
                                                                                                                    Peptide used to determine substrate specificity of an endo-type protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The specification describes an endo-type cysteine protease that has substrate specificity and cleaves the C terminus side of the sequence of Lys-Arg and Arg-Arg. The enzyme has the molecular weight of 72,000 based on SDS-PAGS and an isoelectric point of 5.22. The endo-type cysteine protease is obtained from cod fish milt. The enzyme is used in food and beverage products and pharmaceuticals. The present sequence represents a peptide used to determine specificity of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modulator; sterol-regulated Site-1 protease; cholesterol; sterol regulatory element binding protein; SREBP; lipid synthesis; fatty acid biosynthesis; site-1 protease; protease inhibitor; serum cholesterol; hypercholesterolemia; lipid metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                               New cysteine protease - useful in food/beverage products and
                                                                                                                                            Endo-type cysteine protease; cod fish milt; food; beverage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 84.2%; Score 16; DB 2; Length 4; Local Similarity 75.0%; Pred. No. 1.8e+06; es 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                   note= "protected with -BOC"
                                                                                                                                                                                                                                           /note= "-MAC attached"
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 4; 9pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a peptide.
                                            AAY30777 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                  98JP-00042973
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RVRR 4
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Modified-site
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                                                                                                                                                                    Synthetic
                                                                     AAY30777;
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Matches
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Goldstein JL, Rawson RB;

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Novel assay for identifying modulators of sterol-regulated Site-1 protease useful for the treatment of hypercholesterolemia, involves identifying an agent capable of down regulating Site-1 protease activity.
                                                                                                                                                                                                                                                     The specification describes a method for identifying modulators of a sterol-regulated Site-1 protease. Site-1 protease cleaves sterol regulatory element binding proteins (SREBPs) in the endoplasmic reticulum, initiating release from membranes and activating lipid synthesis. The modulators therefore also modulate cholesterol and fatty acid blosynthesis. The method comprises selecting an agent capable of down regulating Site-1 protease and formulating a composition comprising the agent. The site-1 protease and formulating a composition comprising the agent. The site-1 protease inhibitors are useful for treating a patient for elevated serum cholesterol. Diseases treated include hypercholesterolemia and other lipid metabolism associated conditions. The present sequence was used in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Site-1 protease, SIP, sterol regulatory element binding protein, SREBP, fatty acid synthesis, cholesterol homeostasis, triglyceride.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Site-1 protease inhibition method related peptide #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 16; DB 3; I
Pred. No. 1.8e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                 Example 11; Page 106; 172pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB97408 standard; peptide; 4 AA.
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75.0%;
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WPI; 2002-479626/51.
        WO200127138-A2
                                                                     13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
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                                                                                                                                                                                           homeostasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-APR-2002
                             19-APR-2001
                                                                                                                      Jaen JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE24432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3onny C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAE24432
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
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                                                                                                                                                                                                                                                                                                              The present invention describes a number of peptide derivatives which are capable of modulating Site-1 protease (SIB). SIP initiates the release sterol regulatory element binding proteins (SRBBBs), which control the synthesis of fatty acids and cholesterol. The peptide derivatives of the invention are, therefore, useful in the modulation of cholesterol homeostasis and in the treatment of conditions associated with abnormal levels of plasma cholesterol, lipoproteins or triglycerides. The present sequence is a peptide used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Site-1 protease; SIP; sterol regulatory element binding protein; SREBP; fatty acid synthesis; cholesterol homeostasis; triglyceride.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                              for modulating
                                                                                                                                                                                                                                           Peptide derivatives, useful as SI protease inhibitors for modulati
expression of genes regulated by SREBP transcription factors and f
treating conditions associated with abnormal cholesterol or lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                           /label= OTHER
/note= "modified by 4-methyl-coumaryl-7-amide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= OTHER
/note= "modified by 4-methyl-coumaryl-7-amide"
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 16; DB 4; Length 4;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Site-1 protease fluorigenic peptide assay substrate #10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= OTHER
/note= "modified by t-butyloxycarbonyl"
                                        'note= "modified by t-butyloxycarbonyl"
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                                                                                                                                                                                  UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL.
                                                                                                                                                                                                       Cheng
                                                                                                                                                                                                      Goldstein JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB97427 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                             Example; Page 24; 41pp; English.
                             label= OTHER
                                                                                                                                 11-OCT-2000; 2000WO-US028428
                                                                                                                                                                                                                                                                                                                                                                                                                              84.2%;
75.0%;
                                                                                                                                                    99US-0159236P
                                                                                                                                                                                                       Jaen JC, Li L, Brown MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Conservative
                                                                                                                                                                         (TULA-) TULARIK INC
                                                                                                                                                                                                                         WPI; 2001-328425/34.
                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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| RVRR 4
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                                                                                          WO200127138-A2
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4 AA;
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           Key
Modified-site
                                                  Modified-site
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                                                                                                                                                     13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUL-2001
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                                                                                                              19-APR-2001
                                                                                                                                                                                                                                                                           homeostasis
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AAB97427
XX
AAC AAB9
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XX
DT 27-J
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KW Site
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KW Site
XX
KW Site
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KW Fat
XY
FT Modi
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The present invention describes a number of peptide derivatives which are capable of modulating Site-1 protease (S1P). S1P initiates the release of sterol regulatory element binding proteins (SREBPS), which control the synthesis of fatty acids and cholesterol. The peptide derivatives of the invention are, therefore, useful in the modulation of cholesterol homeostasis and in the treatment of conditions associated with abnormal levels of plasma cholesterol, lipoproteins or triglycerides. The present sequence is a peptide substrate of S1P which can be used in a fluorigenic peptide assay of S1P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transporter peptide; therapy; colon cancer; neurodegenerative disorder; diabetes; respiratory ailment; cardiplegia; viral infection; cytostatic; virucide; neuroprotective.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                Peptide derivatives, useful as S1 protease inhibitors for modulating expression of genes regulated by SREBP transcription factors and for treating conditions associated with abnormal cholesterol or lipid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Pred. No. 1.8e+06;
                                                                                                                                                                                                                  Cheng D;
                                                                                                                                                    (UYTE-) UNIV TEXAS SOUTHWESTERN MEDICAL CENT DAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                  Goldstein JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; Page 27; 41pp; English
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11-OCT-2000; 2000WO-US028428.
                                                          99US-0159236P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 75.0%;
3; Conservative
                                                                                                                                                                                                                  Li L, Brown MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transporter peptide,
                                                                                                                                                                                                                                                                            WPI; 2001-328425/34
                                                                                                                       (TULA-) TULARIK INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RVKR 4
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Gaps ö

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New alpha-amino acid or peptidyl compounds having a C-terminal imidazolesulfonylmethylene group are useful as serine protease inhibitors for treatment of e.g. Alzheimer's disease or multiple organ failure.
                             Claim 35; Page 26; 50pp; English
                                                                                                                                                                                                                               AA014861 standard; protein; 4 AA.
                                                                                                                                                          84.2%;
                                                                                                                                                                                                                                                                                                                                                                          99US-00444883.
                                                                                                                                                                                                                                                                                                                                                                                       ENZY-) ENZYME SYST PROD INC
                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                        3; Conservative
                                                                                                                                                                                                                                                                    Furin substrate peptide.
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-391718/42.
                                                                                                                                                                  Local Similarity
                                                                                                                                                Sequence 4 AA;
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RVRR
                                                                                                                                                                                     1 RVKR
                                                                                                                                                                                                                                                       19-JUL-2002
                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                                                                                                      JS6358928-BL
                                                                                                                                                                                                                                                                                                                                                              22-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                  19-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                   Rasnick DW;
                                                                                                                                                                                                                                            AA014861;
                                                                                                                                                            Query Match
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Matches
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Claim 17; Col 11; 16pp; English

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The invention comprises alpha-amino acid and peptidyl compounds having a C-terminal imidazolesulfonylmethylane group which is a serine protease. inhibitor. The compounds of the invention are capable of interacting with the substrate recognition site of a serine protease. The compounds of the invention are useful for the treatment of diseases characterised by overactivity of one or more serine proteases, e.g. respiratory distress syndrome, septic shock; multiple organ failure; emphyseems; myocardial ischemia; reperfusion injury; dermatitis; cystic fibrosis; chronic bronchitis; arteriosclerosis; Alzheimer's diseases, corneal ulcers; rheumatodid arthritis and acute pancreatitis. The present amino acid sequence represents the furin (serine protease) substrate peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel protein for inducing apoptosis, has proneurotrophin pro-domain with conserved regions, mature neurotrophin domain, and connector that joins conserved region to mature domain and resistant to protease cleavage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated protein comprising a pro-domain (PD) of a proneurotrophin, where PD comprises a pro-domain conserved region, or a modified proneurotrophin protein (Ib) with a PD, a mature neurotrophin domain (MD), and a connector that joins the pro-domain conserved region to MD and resistant to protease cleavage. The PD is selected from specific peptide fragments of human nerve growth factor (NGF), human brain derived neurotrophic factor (BDNF), human neurotrophin 3 (NT-3) or human neurotrophin 4/5 (NT4/5). (ID) is useful for inducing apoptosis in a cell comprising PJS receptors (normal number or higher than the normal number of PJS receptors) on its surface, by causing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 growth factor; NGF; neurotrophin; NT-3; NT4; NT5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                brain derived neurotrophic factor; BDK; vasotropic; carebroprotective; antimicrobial; cardiant; virucide; antimacterial; neuroprotective; nootropic; antiinflammatory; anticonvulsant; plasminogen; plasmin; p75; apoptosis; human.
                                                                                                                                                                                                                                                                                                                                                                                                                        84.2%; Score 16; DB 5; Length 4; 75.0%; Pred. No. 1.8e+06; cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human proneurotrophin cleavage site in BDNF protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kermani
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 13; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABP71148 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Teng KK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORR ) CORNELL RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-MAY-2002; 2002WO-US016540.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-JUL-2001; 2001US-0305510P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAY-2001; 2001US-0293823P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proneurotrophin; nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hempstead BL, Lee R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-140406/13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        Sequence 4 AA;
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                                                                                                                                                                                                                                                                      effector into the cytoplasm and nucleus of a cutaryotic cell preferably a human cell. They are also useful for increasing the intracellular concentration of an effector within a cutaryotic cell, preferably human cell. Transporter peptides of the invention are useful for transporting an effector across a biological membrane, for targeting various cell an effector across a biological membrane, for targeting various cell for increasing the biological activity of the effector to which it is coupled. Pharmaceutical compositions comprising the transporter peptides are useful for treating or preventing diseases such as colon cancer, diabetes, respiratory aliments, neurodegenerative disorders, cardiplegia and viral infections. The present sequence is a transporter peptide of the invention. This peptide can be translocated across a membrane of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Furin substrate; serine protease inhibitor; serine protease substrate recognition site interaction; emphysema; serine protease substrate recognition site interaction; emphysema; respiratory distress syndrome; septic shock; multiple organ failure; myocardial ischemia; reperfusion injury; dermatitis; cystic fibrosis; chronic bronchitis; arteriosclerosis; Alzheimer's disease; corneal ulcer; rheumatoid arthritis; acute pancreatitis.
                    Novel transporter peptide useful for the intracellular delivery of biological effectors for treating diabetes, colon cancer, respiratory ailments, neurodegenerative disorders, cardiplegia, and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                     The present invention relates to novel transporter peptides with the capacity to facilitate transport of an effector across a biological membrane. Sequences of the invention are useful for translocating an
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0
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Pred. No. 1.8e+06;
1; Mismatches 0; Indels
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projection to bind they, in wallings of indicates in the meriod is plaque. The cell is a malignant cell e.g. medulloblastoms or astrocycome) projecte, paracrea, nervous system (e.g. medulloblastoms or astrocycome), prostate, paracrea, nervous system (e.g. medulloblastoms or astrocycome), cleukemia, lymphoma, testicular, lung, brain, malignant oligodendrocyte, heart, vascular smooth muscle or neural cell. A molecule that inhibits the binding of proneurotrophin to a p75 receptor is useful in a method contition associated with undesired apoptosis due to binding of a condition associated with undesired apoptosis due to binding of a condition associated with undesired apoptosis due to binding of a condition associated with undesired apoptosis due to binding of a condition associated with undesired apoptosis due to binding of a condition associated with undesired apoptosis due to binding of a consumental insult. e.g. nervodus system injury, caused by a chemical or radiation or occurring during cancer treatment, hypoxic schemical acused by stroke or heart attack, viral or microbial infection, meningitis, encephalitis or abscesses, neurodegenerative disorders e.g. Alzheimer's disease, familial dysautonomia, ataxia telangictasia, charcet-Marie-Tooth disease, Adreno leuko dystrophy, spinal muscular atrophy or Friedriech's ataxia, or multiple sclerosis, convulsions, epilepsy and spinal cord injury. The present sequence represents the human pronerotrophin cleavage site in BDNF protein mammals or humans. The method is in vitro, in receptor to bind (Ib).

Sequence 4 AA;

Score 16; DB 6; Length 4; Pred. No. 1.8e+06; 1; Mismatches 0; Indels 1; Mismatches 84.2%; 75.0%; 3; Conservative Query Match Best Local Similarity RVKR 4 RVRR 4 Matches 셤 ઠે

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Gaps

0

ADA10587 standard; peptide; 4 AA.

ADA10587;

(first entry) 06-NOV-2003

Eglin c variant related fluorogenic substrate.

protease inhibitor; eglin c variant; reactive loop; acute bacterial; viral; fungal; infection; blocking endoproteolytic activation; bacterial toxin; anthrax toxin protective antigen; diphtheria toxin; pseudomonas aeruginosa exotoxin A; shiga toxin; transgenic animal; fluorogenic; substrate.

Unidentified

'note= "Modified by Boc" /note= "Modified by MCA" Location/Qualifiers Modified-site Modified-site

WO2002102318-A2

27-DEC-2002

18-JUN-2002; 2002WO-US019394.

2001US-0299096P. 2002US-00299096. 18-JUN-2001; 17-JUN-2002;

(UNMI) UNIV MICHIGAN.

Komiyama T, Fuller RS;

WPI; 2003-167438/16.

Composition useful for treating diseases including acute bacterial, viral and fungal infections, has protease inhibitor that is eglin c variant having a non-naturally occurring amino acid in adventitious contact site.

Compound useful as nicotine vaccine comprises molecular adjuvant with

Parameswaran

Thiele GM,

Vennerstrom JL,

SDG,

Sanderson

Srinivasa CR;

Bevins RA,

WPI; 2003-902908/82.

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reversible. This sequence represents a fluorescent substrate peptide used in the creation of first generation eglin c variants of the invention.
                                                                                                                                                                              exposed
                                                                                         further comprising a least one non-naturally occurring and no acid in a reactive loop. The novel composition is useful for treating disease including acute bacterial (e.g. Bacillus anthracis, Corynebacterium diptheriae, and Pseudomonas aeruginosa), viral (respiratory syncytian) virus, measles virus, and human immunodeficiency virus) and fungal (candidiasis and pneumcoystis pneumonia) infections in a patient exposed to an infectious agent. The eglin c variants are useful for blocking endoproteolytic activation of a bacterial toxin including anthrax toxin protective antigen, diphtheria toxin, Pseudomonas aeruginosa exotoxin A purification reagents, as fluorescence tags for identification of cells containing target proteases, for subcellular localisation of proteases, and for tracking internalisation of drugs and for examining and
                                                                                                                                                                                                                                                                                                             inhibiting physiological functions of processing or other proteases in cell cultures or in transgenic animals, for example by selectively inhibiting the enzymes. The eglin c variants are small, stable and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           molecular adjuvant; nicotine hapten; antiaddictive; vaccine; nicotine; smoking; nicotine addiction; immunisation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                          This invention relates to a novel composition comprising a protease inhibitor that is an eglin c variant comprising at least one non-naturally occurring amino acid in an adventitious contact site, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 16; DB 6; Length 4;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetrapeptide protease-sensitive linker SEQ ID NO:19.
               Example 1; Page 76; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD84924 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             84.2%;
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SANDERSON S D G.
VENNERSTROM J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIELE G M.
PARAMESWARAN M.
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SRINIVASA C R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RVKR 4
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                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD84924;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SRIN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 11
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The present invention describes a compound (I) comprising a molecular adjuvant linked to a nicotine hapten. The molecular adjuvant comprises a targeting ligand having binding affinity for an antigen presenting cell.

The targeting ligand is functionally linked to the nicotine hapten so that the binding of the molecular adjuvant to the antigen presenting cell and effecting delivery of the nicotine hapten to an antigen presenting pathway. Also described is a method for the preparation of antibodies to a nicotine hapten comprising an antimal with (I); (b) isolating antibodies from the sera of the animal; and (c) recovering the isolated antibodies from the sera of the animal; and can be used in vaccines. (I) can be used for the treatment or prevention of nicotine addiction via immunisation with a nicotine vaccine. The compound (I) is capable of causing smoking cessation and long term compound (I) is capable of stimularization with an incotine vaccine; necompound (I) is capable of stimularization with an incotine antigen to antigen presenting cells (APCS), and so inducing an anti-nicotine antibody response with little or adjuvants. The present sequence is used in the exemplification of the
targeting ligand linked to nicotine hapten.
                                                             Example 5; SEQ ID NO 19; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 4 AA;
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Gaps ö 84.2%; Score 16; DB 7; Length 4; 75.0%; Pred. No. 1.8e+06; ive 1; Mismatches 0; Indels 3; Conservative Best Local Similarity Query Match Matches

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1 RVKR 4 ઠે

||:| RVRR 4

ADG19004 standard; peptide; 4 AA.

11-MAR-2004 (first entry) ADG19004;

Multimeric transporter peptide related peptide SEQ ID NO:29.

multimeric transporter peptide; transporter peptide; antidiabetic; cytosfetaic; antiliflammatory; nootropic; neuroprotective; virucide; gene therapy; diabetes; colon cancer; respiratory ailment; neurodegenerative disorder; cardioplegia; viral infection.

Synthetic

WO2003103718-A2.

18-DEC-2003

06-JUN-2003; 2003WO-IB003097.

07-JUN-2002; 2002US-00165015.

(UYLA-) UNIV LAUSANNE

Bonny C;

WPI; 2004-062229/06.

New multimeric transporter peptides, useful for treating diabetes, colon cancer, respiratory ailments, neurodegenerative disorders, cardiplegia, and viral infections

Claim 3; SEQ ID NO 29; 49pp; English.

The present invention describes a multimeric transporter peptide (I)

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Also described: (1) a transporter unit comprising the transporter peptide and an effector; (2) translocating the transporter unit across the membrane of pancreatic beta-cells, hepatocytes, muscle cells or lung cells; (3) a pharmaceutical composition comprising the transporter unit and a carrier; (4) a method of producing a translocatable conjugate between the transporter peptide and an effector; (5) a method of increasing the intracellular concentration of an effector with a charmaceutical composition described above; and (7) a method of treating or preventing a disease. (1) has antidiabetic, cytostatic, or preventing a disease. (1) has antidiabetic, cytostatic, antiinflammatory, nootropic, neuroprotective and virucide activities, and can be used in gene therapy. The multimeric transporter peptide (1), compositions and methods of the present invention can be used for treating diabetes, colon cancer, respiratory ailments, neurodegenerative disorders, cardioplegia, and viral infections. The present sequence represents a peptide which can be used as part of a multimeric
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide fragment of alpha-1-antitrypsin, use as convertase inhibitor.
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                                                                                                                                                                                                                                                                                                         84.2%; Score 16; DB 8; Length 4; 75.0%; Pred. No. 1.8e+06; rive 1; Mismatches 0; Indels
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Matches 3; Conservative
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Convertase; inhibitor; alpha-1-antitrypsin; antiinflammatory; vulnerary; ophthalmological; dermatological; nephrotropic; hepatotropic; vasotropic; antiinfertility; respiratory-gen.; cardiant; CNS-gen.; cerebroprotective; neuroprotective; noctropic; cytostatic; antiarthritic; 23-JUL-2003; 2003WO-GB003159 antiarteriosclerotic. WO2004009113-A1 Unidentified. 29-JAN-2004.

24-JUL-2002; 2002GB-00017136 Brunner G; WPI; 2004-180270/17. (RENO-) RENOVO LTD Ferguson MWJ,

manufacture of a medicament for of wounds or reducing fibrosis in Use of a convertase inhibitor in the reducing scarring during the healing the treatment of fibrotic conditions.

Disclosure; Page 10; 43pp;

The present sequence is that of a peptide fragment of alpha-1-antitrypsin. Convertase inhibitors of the invention may be derivatives of alpha-1-antitrypsin comprising this sequence. The inventors have established that convertase enzymes act, both extracellularly and intracellularly, to cause the activation of latent transforming growth factor-beta (TGF-beta) in the extracellular space at the site of a wound

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convertage inhibitors for the reduction of scarring during the healing of wounds, for reducing fibrosis in the treatment of fibrotic conditions, correctating wounds to prevent scar formation, for preventing of the treating wounds to prevent scar formation, for preventing of the eye, nervous tissue or intestines, dermal scarring and scarring of following a burn. The fibrotic condition is a fibrotic disease, achesions glomerulonephritis, cirrhosis of the liver, fibrocytic disease, achesions and restenosis (all claimed). The convertase inhibitor can also be used for the treatment of hypertropic and keloid scars, scarring in the heart, scarring of the gut, scarring in the pelvis in the region of the carring of the gut, scarring in the pelvis in the region of the muscles, scarring or fibrosis following injury to the which can result in serious loss of function, liver fibrosis, pulmonary fibrosis, scleroderma, myocardial hibernation, fibrosis following a stroke or neurodegenerative disorders (e.g. Alzhaimer's disease), proliferative vitreoretinopathy, arthritis, arteriosclerosis and cancer.
fibrotic conditions. Thus, the present invention relates to use of
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Sequence 4 AA;

ö 0; Indels Length 4; Score 16; DB 8; 1 Pred. No. 1.8e+06; 1; Mismatches 0 84.2%; 3; Conservative Query Match Best Local Similarity RVKR 4 Matches 8

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Gaps

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AAR37629 standard; protein; 4 AA. AAR37629; RESULT 14

(revised)
(first entry) 25-MAR-2003 24-SEP-1993 Sequence of proinsulin variant proins.RTKR.Ip having a non-naturally occurring prohormone convertase cleavage site.

Prohormone convertase; enzyme; cleavage; proinsulin; hormone

Synthetic.

WO9311247-A1

10-JUN-1993

92WO-US010621 91US-00803631 04-DEC-1992; 06-DEC-1991;

92US-00887265 22-MAY-1992;

(GETH) GENENTECH INC.

Groskreutz DJ, Sorman CM,

WPI; 1993-197065/24.

Heterologous polypeptide factor prepn. - by introducing into polypeptide factor dependent host cell nucleic acid, and then culturing host cell,

Example; Page 56; 134pp; English.

The inventors describe the production of mammalian cells expressing prohormone convertase which facilitates the processing of prohormone precursors to active hormones. More specifically the cleavage site is the prohormone convertase cleavage site given in AAR37612-35. A human proinsulin mutant having a non-naturally occurring prohormone convertase cleavage site is constructed by mutating the human proinsulin cDNA, pRK.proins encoding the natrually occurring basic cleavage site at the B-

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Gaps

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Indels Length 4;

78.9%; Score 15; DB 2; Le. ilarity 75.0%; Pred. No. 1.8e+06; Conservative 0; Mismatches 1;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The cDNA clone of the human preproinsulin gene, pSVBHIGDHFR, was amplified by primers AAQT1463-4 in a RAGE-PCR. The product was ligated in plasmid pRKS and called pRK.proins. Mutants of the prohormone convertase (PC) cleavage site in the human preproinsulin were constructed (AAAK60591-5) The mutated sites are specifically recognised by murine PC1. The new cleavage sites are labelled either Ip or IIp. Ip is a Type I enzyme cleavage site whereas IIp is a Type II enzyme cleavage site. Cells containing both the prohormone convertase gene and the required precursor gene e.g preproinsulin to be expressed can be injected into a mammal. This system can be used to treat insulin-responsive disorders. (Updated on 25-MAR-2003 to correct PN field.)
               (AAR3/628) by site-directed mutagenesis (Kunkel 1987). The following proinsulin variants were constructed: proins.RTKR.Ip, proins.RQKR.IIp and proins.KTKR.Ip (see AAR3/629-31). The following double proinsulin variants were constructed: proins.KR.Ip/RQKR.IIp and proins.RTKR.Ip/RQKR.IIp. Primers used in proninsulin mutant construction were AAQ43265-67. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Treating insulin-dependent disorders in mammals - by introducing a nucleic acid encoding a variant proinsulin into a host cell with a constitutive pathway of protein secretion, or a plasmid, and introducing the cell or plasmid to the mammal.
chain/C-peptide junction (AAR37627) and/or A-chain/C-peptide junction
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prohormone; convertase; insulin; proinsulin; preproinsulin; factor;
growth; precursors; transgenic; mammal; pcr; primer.
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                                                                                                                                                                                Score 15; DB 2; Length 4;
Pred. No. 1.8e+06;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proins.RTKR.Ip proinsulin mutant cleavage site.
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                                                                                                                                                                                                                                                                                                                                                                                   AAR60593 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                     Perfect score:
                                                                                                                                                                                                                                                                                                                                      Scoring table:
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22, 7 24,

34, 10, 10,

Appli Appli Appli Appli Appli Appli Appli

Appli Appli Appli Appli Appli Appli

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NAME KEY: Modified-site
LOCATION: 1..4
LOCATION: 1..4
OTHER INFORMATION: /label= Modified-sites
OTHER INFORMATION: /note= "The amino terminus is derivatized by a
OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus is
OTHER INFORMATION: derivatized by a 4-methylcoumaryl-7-amide group;"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | Sequence 73, Application US/08460343B |
| Sequence 73, Application US/08460343B |
| Sequence 73, Application US/08460343B |
| Patent No. 5741664 |
| GENERAL INFORMATION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES NUMBER OF SEQUENCES: 7 |
| NUMBER OF SEQUENCES: 7 |
| NUMBER OF SEQUENCES: 7 |
| STREET: 1 DNA Way |
| STREET: 1 DNA Way |
| CITY: South San Francisco |
| STATE: California |
| CONNTRY: USA |
| CONTRY: USA |
| CONTRY: SEADABLE FORM: |
| MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk |
| COMPUTER REDABLE FORM: |
| COMPUTER REDABLE FORM: |
| COMPUTER: IBM PC compatible |
| OPERATION SYSTEM: PC-DOS/MS-DOS |
| CURRENT APPLICATION DATA: |
| APPLICATION NUMBER: US/08/460,343B |
| FILING DATE: 01-Jun-1995 |
| DRICE ADDITION NUMBER: NUMBER: |
| DRICE ADDITION 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.2%; Score 16; DB 1; Length 4; 75.0%; Pred. No. 4.1e+05; tive 1; Mismatches 0; Indels
                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIFICATION: 514
ATTONEY/ASIFICATION: $13003
REFERENCY/DOCKET $35,3003
REFERENCY/DOCKET $1000
TELEPAX: 312-715-1000
TELEPAX: 312-715-1234
TELEFAX: 312-715-1234
TELEFAX: 310-221-5317
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
TENTHH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
TOPOLOGY: linear
                                Illinois
: USA
Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RVRR 4
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                                STATE: I
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US-08-002-202-20
| Sequence 20, Application US/08002202
| Patent No. 5604201
| GENERAL INFORMATION:
| APPLICANT: Thomas, Garry
| APPLICANT: Thomas, Laurel
| APPLICANT: Thomas, Laurel
| APPLICANT: Thomas, Laurel
| TITLE OF INVENTION: Methods and Reagents for Inhibiting
| TITLE OF INVENTION: Purin Endoprotease
| NUMBER OF SEQUENCES: 21
| CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               US-08-002-202-4
; Sequence 4, Application US/08002202
; Patent No. S604201
; Patent No. S604201
; APPLICANT: Thomas, Garry
; APPLICANT: Thomas, Laurel
; APPLICANT: Thomas, Laurel
; APPLICANT: Hayflick, Joel S
; TITLE OF INVENTION: Methods and Reagents for Inhibiting
; TITLE OF INVENTION: Purin Endoprotease
; UNWERR OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.2%; Score 16; DB 1; Length 4; 75.0%; Pred. No. 4.1e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USAN
ZIP: 6666
COMPUTER 18ADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIFICATION INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5664201nan, Kevin B
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,448
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAMINICATION INFORMATION:
TELECAMINICATION INFORMATION:
TELECAMINICATION OF 312-715-1000
TELECAMINICATION OF 312-715-1034
TELECAMINICATION OF SEQ 1D NO: 4:
SEQUENCE CHARACTERISTICS:
FENCTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
                                                                    ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||:|
RVRR 4
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Gaps

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UMBER: 08/398028 03-mar-1995

PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08
FILING DATE: 03-mar-194

B: Allegretti and Witcoff, Ltd. 10 South Wacker Drive, Suite 3000

ADDRESSEE: STREET: 10

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| Sequence 4, Application US/08481534 |
| Patent No. 6022855 |
| GENERAL INFORMATION: |
| APPLICANT: Thomas, Gary |
| APPLICANT: Thomas, Laurel |
| APPLICANT: Thomas, Laurel |
| APPLICANT: Hayflick, Josel 8 |
| APPLICANT: Hayflick, Josel 8 |
| APPLICANT: Stenglen, Stephan G |
| APPLICANT: Stenglen, Stephan G |
| TITLE OF INVENTION: Endoprotease |
| NUMBER OF SEQUENCES: 21 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff |
; Sequence 73, Application US/08504265B
; Patent No. 5837516
; GENERAL INFORMATION:
    APPLICANT: Marcus D. Ballinger and James A. Wells
    TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
    TUTLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
    TITLE OF INVENTION: SUBSTRATES CONTAINING BASIC RESIDUES
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: Genentech, Inc.
    STREET: I DNA WAY
    CITY: South San Francisco
    STATE: California
    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16; DB 2; Length 4;
Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
                                                                                                                                                                                                                                                                                               ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IEBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winheatin (Genentech) CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,265B FILING DATE: 19-Jul-1995 CLASSIFICATION 335 PRIOR APPLICATION DATA:
APPLICATION DATE: 19-Jul-1995 FILING DATE: 03-MAR-1995 FILING DATE: 03-MAR-1995 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P0936P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P09;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-8228
TELEPHONE: 650/952-981
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 3; Conserv
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STREET: 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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US-08-481-534-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 73, Application US/08398028B
Patent No. 5780285
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAR WAY
                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.2%; Score 16; DB 1; Length 4; 75.0%; Pred. No. 4.1e+05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                               DB 1; Length 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITYER: South San Francisco
STATE: California
COUNTRY: JUSA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,028B
FILING DATE: 03-Mar-1995
CLASSIPTCATION WINMER: US/08/398,028B
FILING DATE: 03-Mar-1995
CLASSIPTCATION NUMBER: 36,575
REFERENCE CONTEXT UNFORMATION:
NAMB: KUDINGC, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE CONTEXT UNFORMATION:
TELEPHONE: 650/225-8228
TELEPHONE: 650/252-9821
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           84.2%; Score 16; DB 1; I
75.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
    ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REPERENCE/DOCKET NUMBER: 90936C1
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/252-981
TELEFAX: 650/252-981
TELEFAX: 650/252-981
TELEFAX: 4 amino acide
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 75.0
The 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-398-028B-73
                                                                                                                                                                                                                                                     ; TOPOLOGY: Linear
US-08-460-343B-73
                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:|
RVRR 4
                                                                                                                                                                                                                                                                                                                                                                                                                   1 RVKR 4
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US-08-504-265B-73
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US-08-398-028B-73
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Gaps

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APPLICANT: SCHLOKAT, Uwe
APPLICANT: SCHLOKAT, Uwe
APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Bernhard
APPLICANT: FISCHER, Earlo-Guenther
APPLICANT: BIBL, Johann
TITLE OF INVENTION: A FUSION PROTEIN COMPRISING A FURIN
TITLE OF INVENTION: BERIVATIVE OR A DERIVATIVE OF A FURIN
TITLE OF INVENTION: HETREOLOGOUS SEQUENCE
TITLE OF INVENTION: HETREOLOGOUS SEQUENCE
CORRESPONDENCE ADDRESS:
ANDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STREET: 20007-5109
CONFUTRY: USA
ZIP: 20007-5109
COMPUTER: READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,247
FILING DATE: 22-NOV-1996
CLASSIFICATION: 435
                                                                                                                                / note="The amino terminus us derivatized by a butoxycarbonyl group, and the carboxyl terminus is derivatized by a 4-methylcoumaryl-7-amide group."
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                                                                                                                                                                                                                                              84.2%; Score 16; DB 3; Length 4; 75.0%; Pred. No. 4.1e+05; ive 1; Mismatches 0; Indels
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                                                                                                                /label=Modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40433/149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT 1928/95
FILING DATE: 24-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 49433/14
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29, Application US/08753247
Patent No. 6210929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              th 84.2%; Similarity 75.0%; 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 29
SEQUENCE CHARACTERISTICS:
                     MOLECULE TYPE: peptide FRATURE: NAME/KEY: Modified site
                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 4 amino acids
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                                                                                    LOCATION: 1..4
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
  TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 3; Conserv
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           1 RVKR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                    US-08-481-534-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-08-753-247-29
                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08481534

Patent No. 6022855

GENERAL INFORMATION;
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Endoprotease
NUMBER OF INVENTION: Endoprotease
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.2%; Score 16; DB 3; Length 4; 75.0%; Pred. No. 4.1e+05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IS Floppy disk
COMPUTER: ISM PC compatible
COMPTIER: ISM PC compatible
COMPTIER: ISM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,534
FILING DATE: 14-SEP-1995
CLASSIFICATION: S30
ATTORNEY/AGENT INFORMATION:
NAME: No. 6022855nan, Kevin E
REGISTRATION NUMBER: 92,448-D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                SCETALING SILEM.
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,534
FILING DATE: US/08/481,534
FILING DATE: US/08/481,534
ATMONEY/AGENT INFORMATION:
NAME: No. 630
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D
TELEPROMUNICATION INFORMATION:
TELEPRAMINE: 312-913-0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B: McDonnell Boehnen Hulbert & Berghoff
300 South Wacker Drive
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 75.0 Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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1 RVRR 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-481-534-20
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Gaps

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Sequence 3, Application US/09444883
Facert No. 6358928
GENERAL INFORMATION:
APPLICANT: Raenick, David W.
TITLE OF INVENTION: BEFTIDYL SULFONYL IMIDAZOLIDES AS SELECTIVE INHIBITORS OF TITLE OF INVENTION: BEFTIDYL SULFONYL IMIDAZOLIDES AS SELECTIVE INHIBITORS OF TITLE OF INVENTION: BEFTIDE PROTEASES
FILE REFERENCE: 6095-5
CURRENT APPLICATION NUMBER: US/09/444,883
CURRENT FILING DATE: 1999-11-22
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Sequence 33, Septilization US/09640198D

SENERAL INFORMATION:
APPLICANT: Kay Whye, Peng
TITLE OF INVENTION: System for Monitoring the Location of
TITLE OF INVENTION: System for Monitoring the Location of
TITLE OF INVENTION: System for Monitoring the Location of
TITLE OF INVENTION: System for Monitoring the Location of
TITLE OF INVENTION: System for Monitoring the Location of
TITLE OF INVENTION: System for Monitoring the Location of
TITLE OF INVENTION: System for Monitoring the Location of
TOTAL OF INVENTION: System for Monitoring the Location of
SPERON FILING DATE: 1999-08-17

NUMBER OF SEQ ID NOS: 34

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 33

LENGTH: 4
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Pred. No. 4.1e+05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.2%; Score 16; DB 3; Length 4; illarity 75.0%; Pred. No. 4.1e+05; Conservative 1; Mismatches 0; Indels
   Similarity 75.0%; Pred. No. 4.1e+05; 3; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Binding Site for Furin US-09-444-883-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FEATURE:
; OTHER INFORMATION: Cleavable Linker Site
US-09-640-198D-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 3, Application US/09639667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84.2%;
75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 3; Conserv
Best Local Similarity
Matches 3; Conserv
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||:|
1 RVRR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-640-198D-33
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US-09-444-883-3
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US-09-639-667-3
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                                                                                                                                                         US-09-360-237-40

| Sequence 40, Application US/09360237
| Patent No. 6322962
| GENERAL INFORMATION:
| APPLICANT: BROWN, MICHAEL S.
| APPLICANT: ESPENSHADE, PETER J.
| APPLICANT: ESPENSHADE, PETER J.
| APPLICANT: SEPENSHADE, PETER J.
| APPLICANT: APPLICANT: STREAL, UGSEPH L.
| APPLICANT: APPLICANT: STREAL, USOS J.
| APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: MODULATORS THEREOF
| TITLE OF INVENTION: MODULATORS THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 54, Application US/09360237

Sequence 54, Application US/09360237

Patent No. 6322962

GENERAL INFORMATION:

APPLICANT: BENGW, MICHAEL S.

APPLICANT: GENGW, MICHAEL S.

APPLICANT: GENGLY: DONG

APPLICANT: GENGLY: OSEPH L.

APPLICANT: SAKAI, JUNO

TITLE OF INVENTION: STEROL-REGULATED SITE-1 PROTEASE AND ASSAYS OF

TITLE OF INVENTION: UNDER: UNDIATORS THEREOF

TITLE OP INVENTION: UNDER: US/09/360,237

CURRENT APPLICATION UNDER: 09/99-07-23

CURRENT PILLING DATE: 1999-07-23

EARLIER APPLICATION UNDER: 60/096,571

SARLIER PILING DATE: 1998-08-14

NUMBER OF SEQ ID NOS: 60

SEQ ID NO 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC OTHER INFORMATION: PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           84.2%; Score 16; DB 3; Length 4; 75.0%; Pred. No. 4.1e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.2%; Score 16; DB 3; Length 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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1 RVRR 4
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US-09-360-237-54
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1 RVKR 4
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TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
## SERVERAL INFORMATION:
| JAPRILCANT: RUBBELL, Stephen James |
| APPLICANT: RUBBELL, Stephen James |
| APPLICANT: RUBBELL, Stephen James |
| APPLICANT: Peng, Kah Whye |
| TITLE OF INVENTION: SYSTEM FOR WONITORING THE EXPRESSION OF ITILE OF INVENTION: TRANSGENES |
| FILE REPERENCE: 07039-292001 |
| CURRENT APPLICATION NUMBER: US/09/639,667 |
| FRICK APPLICATION NUMBER: 60/149,168 |
| PRIOR APPLICATION NUMBER: 60/149,168 |
| PRIOR FILING DATE: 1999-08-17 |
| NUMBER OF SEQ ID NOS: 31 |
| SOFTWARE: FastESEQ for Windows Version 4.0 |
| SEG ID NO 3 |
| SEG ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.9%; Score 15; DB 1; Length 4; 75.0%; Pred. No. 4.1e+05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 16; DB 4; Length 4; Pred. No. 4.1e+05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILING DATE: 23-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: 31,5201-FWC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 36, Application US/08200900A Patent No. 5665566 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                  ; FEATURE:
; OTHER INFORMATION: linker peptide
US-09-639-667-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 78.9
Best Local Similarity 75.0
Matches 3; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:||
RLKR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RVKR 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 14
US-08-200-900A-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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Gaps
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                                                                                                                        CLONING OF ENTEROKINASE AND METHOD OF USE
                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILLING DATE: U3-FEB-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Meiner, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-5851
TELEPHONE: (617) 876-5851
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 4;
                                                                                                                  TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOI NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: Genetics Institute, Inc. - Legal Affairs STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 15; DB 1; I
Pred. No. 4.1e+05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: June 20, 2005, 16:35:40 Job time : 30 secs
                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Sequence 38, Application US/08200900A Patent No. 5665566 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78.9%;
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Best Local Similarity 75.0
Matches 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                           ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                   STATE: MA
COUNTRY: USA
ZIP: 02140
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RESULT 15
US-08-200-900A-38
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Sequence 17, Appli
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Sequence 9, Appli
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Sequence 17, Appl
Sequence 38, Appl
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Sequence 22, Appl
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Sequence 54, Appl
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Sequence 3, Appli
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11, Appl
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1178, Ap
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             Sequence 26, Sequence 60, Sequence 15, Sequence 38, Sequence 5, Al Sequence 14, Al Sequence 11, Al Sequence 11, Sequence 11,
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Sequence 11, R
Sequence 19, R
Sequence 19, R
Sequence 17, R
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\tt a_{constraint}
   Sequence 3, Appli
Sequence 8, Appli
Sequence 29, Appl
Sequence 29, Appl
Sequence 24, Appl
Sequence 29, Appl
Sequence 3, Appl
Sequence 12, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 23, Appl
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                                                                               June 20, 2005, 16:33:52; Search time 104 Seconds (without alignments) 14.768 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
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(cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: +
(cgn2_6/ptodata/2/pubpaa/USG6_PUBCOMB.pep: +
(cgn2_6/ptodata/2/pubpaa/USG6_PUBCOMB.pep: +
(cgn2_6/ptodata/2/pubpaa/USG6_PUBCOMB.pep: +
(cgn2_6/ptodata/2/pubpaa/USG8_PUBCOMB.pep: +
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(cgn2_6/ptodata/2/pubpaa/USG0_PUBCOMB.pep: +
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Compugen Ltd.
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US-10-478-179-8
US-10-165-015-29
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US-10-155-886-24
US-10-58-866-33
US-10-399-127-29
US-10-641-834-3
US-09-881-669-12
US-09-881-669-12
US-09-891-6868-22
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             version - 2005
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Maximum Match 100%
Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
                                                          protein search, using sw
             GenCore
Copyright (c) 1993
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Match
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Sequence 29, Application US/10165015

Publication No. US20030032594A1

GENERAL INFORMATION:

APPLICANT: PATT, Tech Transfer Office University of Lausanne

APPLICANT: Bonny, Christopher DELIVERY OF BIOLOGICAL EFFECTORS

TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS

TITLE OF INVENTION: 10049-512 CIP

CURRENT APPLICATION NUMBER: US/10/165,015

CURRENT FILING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: 09/977,831

PRIOR APPLICATION NUMBER: 60/240,315

PRIOR APPLICATION NUMBER: 60/240,315

NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 29, Application US/09977831
; Sequence 29, Application US/09977831
; Patent No. US20020120100A1
; GENERAL INFORMATION:
; APPLICANT: PACTT, Tech Transfer Office University of Lausanne
; APPLICANT: Bonny, Christophe
; TITLE OF INVENTION: INTRACELLUIAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 Transporter peptides
; CURRENT APPLICATION NUMBER: US/09/977,831
; CURRENT APPLICATION NUMBER: US.S.N. 60/240,315
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                     Gaps
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Similarity 100.0%; Score 19; DB 16;
Similarity 100.0%; Pred. No. 1.5e+06;
4; Conservative 0; Mismatchica
CURRENT FILING DATE: 2003-11-18
PRIOR APPLICATION NUMBER: PCT/US02/15992
PRIOR FILING DATE: 2002-05-20
PRIOR PILING DATE: 2002-05-18
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                      OTHER INFORMATION: linker peptide
                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 4; Conserv
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Best Local Similarity
Matches 3; Conserv
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US-09-977-831-29
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                                                                                                                                                             LENGTH: 4
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Publication No. US20040127396A1
Publication No. US20040127396A1
REBERRAL INFORMATION:
AEPLICANT: DUBOIS, Claire
TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
TITLE OF INVENTION: USE OF FURIN AND FURIN REMODELLING DISEASES
FILE REPERENCE: 85761-28
CURRENT APPLICATION NUMBER: US 60/213,995
PRIOR PEDICATION NUMBER: CA 2,312,109
PRIOR PEDICATION NUMBER: CA 2,312,109
PRIOR APPLICATION NUMBER: CA 2,312,109
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin Version 3.2
SEQ ID NOS: 3
SOFTWARE: Patentin Version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: MOD_RES
1 LOCATION: (4)...(4)
2 LOCATION: Arg at position 4 is modified at its carboxyl group with a -CH2Cl US-09-885-9148-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Arg at position 1 is modified at its amino group with a decanoyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Sequence 1
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100.0%; Pred. No. 1.5e+06;
iive 0; Mismatches 0;
    US-10-751-699-82
US-10-76-326-35
US-10-841-787-1
US-10-841-787-1
US-10-841-787-1
US-10-841-056-12
US-10-841-056-12
US-10-841-056-12
US-10-433-709-12
US-10-715-976-35
US-10-503-910-38
US-10-227-110-18
US-10-227-110-18
US-10-227-110-18
US-10-237-110-18
US-10-237-110-18
US-10-237-110-18
US-10-237-110-18
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US-10-478-179-8
US-10-478-179-8

Squence 8, Application US/10478179

Publication No. US20040249126A1

GENERAL INFORMATION:
APPLICANT: Cells, Esteban

TITLE OF INVENTION: CHIMERIC ANTIGEN-SPECIFIC T

TITLE OF INVENTION: CELL-ACTIVATING POLYPEPTIDES

FILE REFERENCE: 07039-277US1

CURRENT APPLICATION NUMBER: US/10/478,179
                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 4; Conservative
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            LENGTH:
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Score 16; DB 16;
Pred. No. 1.5e+06;
                                                                                                                                                                                                                                                  ; Sequence 29, Application US/10399127; Publication No. US20040110690A1; GENERAL INFORMATION:
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                                          84.2%;
75.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.2%;
                                        Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:|
1 RVRR 4
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US-10-399-127-29
     US-10-428-868-33
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                                                                                           FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER
FORTHER OTHER INFORMATION: PEPTIDE
US-10-165-015-29
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TITLE OF INVENTION: System for Monitoring the Location of
TITLE OF INVENTION: Transgenes
FILE REPERENCE: 07039-295001
CURRENT APPLICATION NUMBER: US/10/428,868
CURRENT FILING DATE: 2003-05-01
PRIOR PILING DATE: 2000-08-16
PRIOR PILING DATE: 2000-08-16
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 34
NUMBER OF SEQ ID NOS: 34
                                                                                                                                                                                       Score 16; DB 14; Length 4;
Pred. No. 1.5e+06;
1; Mismatches 0; Indels
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Pred. No. 1.5e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/10155886
FUDLICATION NO. US20030087804A1
GENERAL INFORMATION:
APPLICANT: Hempstead, Barbara L.
APPLICANT: Teng, Kenneth K.
APPLICANT: Teng, Kenneth K.
APPLICANT: Remain, Pounch
TITLE OF INVENTION: High Affinity Ligand For p75;
FILE REPRENCE: 955-21 Sequence No. US2003008786;
CURRENT APPLICATION UNMERR: US/10/155,886
CURRENT FILING DATE: 2002-08-05
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Publication No. US20030235332A1
GENERAL INFORMATION:
APPLICANT: Russell, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2002-08-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.28;
                                                                                                                                                                                     Similarity 75.0%;
3; Conservative
                                                      TYPE: PRT
ORGANISM: Artificial Sequence
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
LENGTH: 4
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
Matches 3; Conserv
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ORGANISM: Unknown
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RVRR 4
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RVRR 4
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US-10-428-868-33
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                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOIND, Christophe
TITLE OF INVENTION: INTRACELLULAR DELIVERY OF BIOLOGICAL EFFECTORS
FILE REFERENCE: 20149-512 NATL
CURRENT APPLICATION NUMBER: US/10/399,127
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: 60/240,315
PRIOR APPLICATION NUMBER: 60/240,315
PRIOR PILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 29
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Sequence 3, Application US/10641834

Publication No. US20040209830A1

GENERAL INFORMATION:

APPLICANT: Russell, Stephen James

APPLICANT: Peng, Kah Whye

TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF

TITLE OF INVENTION: TRANSGENES

TITLE OF INVENTION: TRANSGENES

TITLE OF INVENTION: TRANSGENES

CURRENT APPLICATION NUMBER: 05/63,667

PRIOR FILING DATE: 2003-05-18

PRIOR FILING DATE: 1999-08-16

PRIOR FILING DATE: 1999-08-16

PRIOR FILING DATE: 1999-08-17

NUMBER OF SEQ ID NOS: 31

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 4
Score 16; DB 15; Length 4;
Pred. No. 1.5e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 4;
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Pred. No. 1.5e+06;
1; Mismatches 0
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Length 4;

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Gaps

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0; Indels

Mismatches

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3; Conservative

Matches

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Gaps
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                                                                                                                                        Score 15; DB 9; Length 4;
Pred. No. 1.5e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/997,868
FILING DATE: 12-Mar-2002
CLASSIFICATION AUMBER: US/09/997,868
FILING DATE: 12-Mar-1002
PRIOR APPLICATION NUMBER: 07/891265
FILING DATE: 22-May-1992
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
APPLICATION NUMBER: 07/803631
FILING DATE: 06-DEC-1992
APPLICATION NUMBER: PCT/US92/10621
FILING DATE: 04-DEC-1992
ATTORNEY/AGRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78.9%; Score 15; DB 10; 75.0%; Pred. No. 1.5e+06; iive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22, Application US/09997868
Publication No. US20031031654A1
GENERAL INFORMATION:
APPLICANT: Gorman, Cornella M.,
GROSKreutz, Debyra J.
TILE OF INVENTION: Prohormone Convertase
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (0)...(0)
; CHERR INFORMATION: proteolytic processing site
US-09-841-730-23
                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0748P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
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ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: South San Francisco
STATE: California
COUNTRY: USA
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INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                           78.9%;
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                                                                                                                                           Query Match 78.9
Best Local Similarity 50.0
Matches 2; Conservative
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US-09-641-730-23

Sequence 23, Application US/09841730

Patent No. US20020157126A1

GENERAL INFORMATION:

APPLICANT: McPherron, Alexandra C.

TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME

FILE REFERENCE: JHU1470-2

CURRENT APPLICATION NUMBER: US/09/841,730

CURRENT APPLICATION NUMBER: 09/626,896

PRIOR FILING DATE: 2000-07-27

PRIOR PELING DATE: 2000-01-31

PRIOR FILING DATE: 2000-01-31

PRIOR FILING DATE: 1998-07-28

PRIOR FILING DATE: 1998-07-28

PRIOR FILING DATE: 1998-07-38

PRIOR FILING DATE: 1998-07-89

PRIOR FILING DATE: 1998-07-89

PRIOR FILING DATE: 1998-07-80

PRIOR FILING DATE: 1998-07-80

PRIOR FILING DATE: 1999-07-80
                                                                                                                                                                                             Sequence 12, Application US/09887669

Fublication No. US20020082397A1

GENERAL INFORMATION:

APPLICANT: SCHESSINGER, JOSEPH

APPLICANT: SCHESSINGER, JOSEPH

APPLICANT: ULLRICH, AXEL

APPLICANT: UNCELNOR

APPLICANT: WOREL, WOLFGANG

APPLICANT: BOGGL, 1246

CURRENT APPLICATION NUMBER: US/09/887, 669

CURRENT APPLICATION NUMBER: US/09/87, 244

PRIOR FILING DATE: 1993-07-01

PRIOR FILING DATE: 1993-07-01

PRIOR FILING DATE: 1993-04-21

NUMBER OF SEQ ID NOS: 13

SOSTWARE: PATENTIN VET: 2.1
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Pred. No. 1.5e+06;
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 75.0%;
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ORGANISM: Eukaryotes
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TYPE: PRT
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  Sequence 23, Application US/10013032

Sequence 23, Application US/10013032

Publication No. US20020155544A1

GENERAL INFORMATION:

APPLICANT: Hollet, Debra A

APPLICANT: Alam, Tausif

APPLICANT: Sollinger, Hans W.

ITILE OF INVENTION: Treatment of Diabetes with Synthetic Beta Cells

FILE REFERENCE: 96429/9003CIP

CURRENT APPLICATION NUMBER: US/10/013,032

CURRENT PILING DATE: 2002-05-01

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/537,696

PRIOR PILING DATE: EARLIER FILING DATE: 2000-03-28

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 24

SOPTWARE: PATENTING DATE: EARLIER FILING DATE: 1998-07-15

SEQ ID NOS: 24

SSP ID NOS: 24
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TITLE OF INVENTION: METHODS OF TREATING BLADDER DISORDERS
FILE REPERENCE: 08191-022001
CURRENT APPLICATION NUMBER: US/10/074,956
CURRENT PILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/268,175
PRIOR PILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 26
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Publication No. US20020193332A1
GENERAL INFORMATION:
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Publication No. US20030223977A1
GRNERAL INFORMATION:
APPLICANT: LEY, Arthur Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 50.۰۰
نم 2; Conservative
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US-10-115-134-60
US-10-013-032-23
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Sequence 15. Application US/10831302
| Sequence 15. Application US/10831302
| Publication No. US20050003482A1
| GENERAL INFORMATION:
| APPLICANT: Fang, Jianmin
| APPLICANT: Joose, Karin
| APPLICANT: Joose, Karin
| TITLE OF INVENTION: Compositions and Methods for Enhanced Expression of
| TITLE OF INVENTION: Cleavage Site
| TITLE OF INVENTION: Cleavage Site
| TITLE OF INVENTION: Lleavage Site
| TITLE OF INVENTION: Lleavage Site
| FILE REFERENCE: 3802-092-27CIP
| CURRENT FILING DATE: 2004-04-26
| PRIOR APPLICATION NUMBER: US 10/452,253
| PRIOR APPLICATION NUMBER: US 60/540,554
| PRIOR FILING DATE: 2004-02-02
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 15
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APPLICANT: GUTERMAN, Sonia Kosow

APPLICANT: MRKLAND, William

APPLICANT: KENT, Rachel Baribault

APPLICANT: KENT, Rachel Baribault

APPLICANT: ROBERTS, Bruce Lindsay

APPLICANT: LADINER, Robert Charles

TILLE OF INVENTION: DOMAIN MUTANTS AS CATHEPSIN G INHIBITORS

FILE REFERENCE: LEFIN SOLIN NUMBER: US/10/115,134

CURRENT APPLICATION NUMBER: 08/49,406

PRIOR APPLICATION NUMBER: 08/849,406

PRIOR PILING DATE: 2001-07-21

NUMBER OF SEQ ID NOS: 92

SOFTWARE: Patentin Version 3.2

SEQ ID 060
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Pred. No. 1.5e+06;
0; Mismatches 1
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Pred. No. 1.5e+06;
0; Mismatches 1.
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US-10-831-302-15
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COTHER INFORMATION: 39-42 OF BRINK

US-10-115-134-60
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78.9%;
Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 75.0%;
Matches 3; Conservative
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ORGANISM: Artificial
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Sequence 19, Appl
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Sequence 13, Appl
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Sequence 12, Appl
Sequence 21, Appl
Sequence 36, Appl
Sequence 86, Appl
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Sequence 22, Appl
Sequence 26, Appl
Sequence 60, Appl
Sequence 61, Appl
Sequence 15, Appl
Sequence 38, Appl
Sequence 26, Appl
Sequence 34, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 74, Appl
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Sequence 13,
Sequence 15,
Sequence 23,
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                                    B
                 Length
Query
Match
                                                                                                                                                                                                                                                                         Score
                                          Result
No.
                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                           20, 2005, 16:24:07; Search time 328.5 Seconds (without alignments) 14.222 Million cell updates/sec
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1: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
13: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
14: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
15: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
16: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
18: /cgn2_6/ptodata/1/paa/US0976_COMB.pep:*
19: /cgn2_6/ptodata/1/paa/US0976_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US0976_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US0976_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US0976_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US0976_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US0976_COMB.pep:*
10: /cgn2_6/ptodata/1/pa
                                                                                                                                                                                                                                                61006
  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /paa/US108_COMB.pep.
                                                                                                                                                                                                                                             hits satisfying chosen parameters:
                                                                                                                                                                                                                      6959266 seqs, 1168006243 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                    protein search, using sw model
                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
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19
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PCT-USO2-19394-69
; Sequence 69, Application PC/TUS0219394
; GENERAL INFORMATION:
    APPLICANT: Komiyama, Tomoko
; APPLICANT: Komiyama, Tomoko
; APPLICANT: Komiyama, Tomoko
; TITLE OF INVENTION: Eglin Resed Drugs for Treatment of Disease
; TITLE OF INVENTION: BGJIN NUMBER: PCT/US02/19394
; CURRENT APPLICATION NUMBER: 2003-02-07
; PRIOR APPLICATION NUMBER: 60/299,096
; RIOR FILING DATE: 2001-06-18
; NUMBER: OF SEQ ID NOS: 70
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ô
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PCT-US03-05015-19
; Sequence 19, Application PC/TUS0305015
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Nebraska
                                                 US-10-478-179-8

Sequence 8, Application US/10478179

Sequence 8, Application US/10478179

GENERAL INFORMATION:

APPLICANT: Celis, Esteban

TITLE OF INVENTION: CHIMERIC ANTIGEN-SPECIFIC T

TITLE OF INVENTION: CELL-ACTIVATING POLYPEPTIDES

FILE REFERENCE: 07039-277US1

CURRENT FALING DATE: 2003-11-18

PRIOR APPLICATION NUMBER: PCT/US02/15992

PRIOR APPLICATION NUMBER: US 60/291,874

PRIOR APLICATION NUMBER: US 60/291,874

PRIOR PILING DATE: 2001-05-18

NUMBER: OF SEQ ID NOS: 38

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 19; DB 30;
Similarity 100.0%; Pred. No. 6.4e+06;
4; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: linker peptide US-10-478-179-8
                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity
Matches 4; Conserv
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1 RVKR 4
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1 RVRR 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09885914B
Sequence 3, Application US/09885914B
GENERAL INFORMATION:
TAPLICANT: DUBCIS, Claire
TITLE OF INVENTION: USE OF FURIN AND FURIN-LIKE PROTEASE INHIBITORS IN THE TREATMENT
TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
TITLE OF INVENTION: OF INFLAMMATORY OR MATRIX REMODELLING DISEASES
CURRENT PELLON NUMBER: US/09/885,914B
CURRENT PILING DATE: 2001-06-22
PRIOR PELLON NUMBER: CA 2,312,109
PRIOR FILING DATE: 2000-06-23
NUMBER: OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MOD RES
LOCATION: (4)...(4)
OTHER INFORMATION: Arg at position 4 is modified at its carboxyl group with a -CH2Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)..(1)
OTHER INFORMATION: Arg at position 1 is modified at its amino group with a decanoyl
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Appli
Sequence 1, Appli
Sequence 56, Appl
   Sequence 34, Appl
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Sequence 28, Appl
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Appl
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                                                                                                                                                                                                                                  Sequence 6, A Sequence 23, Sequence 56, Sequence 23, Sequence 17, Sequence 17, Sequence 20,
                            Sequence 43,
Sequence 30,
Sequence 49,
                                                                        Sequence 38,
Sequence 1,
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                  Sequence
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Sequence
Sequence
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         US-10-125

US-10-895-064-2596

PCT-US02-02814-43

PCT-US02-02814-49

PCT-US02-21-14-49

PCT-US02-283-97-1

PCT-US02-283-97-1

PCT-US03-3812-11

PCT-US04-11481-17

PCT-US04-11481-17

PCT-US04-11482-17

PCT-US04-2191-20

PCT-US04-2191-20

PCT-US04-2191-20

PCT-US04-2191-20

PCT-US04-23191-20

PCT-US08-2339-56

US-08-244-121-23

US-08-244-121-23

US-08-385-207-20
                                                                                                                                                                                                                                                                                                                                                   US-08-814-394A-9
US-09-006-298-28
US-09-011-006C-52
US-09-049-770-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Synthetic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 4; Conservative
                                           NAME/KEY: MOD_RES
LOCATION: (1)..(1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-885-914B-3
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Gaps

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APPLICANT: Marcus D. Ballinger and James A. Wells
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: CLEAVING SUBSTRATES CONTAINING BASIC RESIDUES
NUMBER OF SEQUENCES: 89
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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                                                                                                                                                                                                                                                                                         APPLICANT: Marion:
TITLE OF INVENTION: SUBTILISIN VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: South San Bruno Blvd
CITY: South San Francisco
STATE: California
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4;
Pred. No. 6.4e+06;
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Pred. No. 6.4e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS SOCREATING SYSTEM: PC-DOS/MS-DOS SOCREENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,343A FILING DATE: 01-Jun-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/398028
FILING DATE: 03-mar-1995
ATORNEY/AGENT INFORMATION:
NAME: KUDINEC, JEffrey S.
REGISTRATION NUMBER: 36,575
                                                                                                                                                                                                                                                   Sequence 73, Application US/08460343A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 73, Application US/08504265A; GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
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                   75.0%;
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Best Local Similarity 75.0
Matches 3; Conservative
                                             3; Conservative
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TOPOLOGY: Linear
                Best Local Similarity
Matches 3; Conserv
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US-08-504-265A-73
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                                                                                           ઠે
                                                         APPLICANT: Thiele, Geoffery M.
APPLICANT: Thiele, Geoffery M.
APPLICANT: Parameswaran, Maniyan
APPLICANT: Bevins, Rick A.
APPLICANT: Bevins, Rick A.
APPLICANT: Bevins, Rick A.
APPLICANT: Stinivasa, Cheruku R.
APPLICANT: Stinivasa, Cheruku R.
TITLE OF INVENTION: Compositions and compounds for use as a
TITLE OF INVENTION: antigen-presenting cell receptor as a molecular adjuvant
TITLE OF INVENTION UNMER: PERSONALION NUMBER: PCT/US03/05015
CURRENT PILING DATE: 2003-02-20
RICK APPLICATION NUMBER: 60/360,967
RICK APPLICATION NUMBER: 60/360,967
RICK APPLICATION NUMBER: 2003-03-01
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PRESENCE OF Windows Version 3.0
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GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 16; DB 1; Length 4;
Pred. No. 6.4e+06;
1; Mismatches 0; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,028A
FILING DATE: 03-Mar-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0936
TELECOMMUNICATION INFORMATION:
TELECHONE: 415/25-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /3
// AUDRESS:

JUBET: Genentech, Inc.
JUBET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic Sequence PCT-US03-05015-19
                                           Vennerstrom, Jonathan L.
Thiele, Geoffery M.
Parameswaran, Maniyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%;
Matches 3; Conservative 1
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ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
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RVRR 4
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US-08-398-028A-73
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                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 19
LENGTH: 4
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LOCATION: 1..4
OTHER INFORMATION: /label=Modified site
OTHER INFORMATION: / note="The amino terminus us derivatized by a
OTHER INFORMATION: butoxycarbonyl group, and the carboxyl terminus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Reject of the term of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
FILING DATE: 14-SP-1995
ATFORNEY/AGENT INPORMATION:
PRIOR APPLICATION NUMBER: US/09/372,003
REPERENCE/POCKET NUMBER: 35,303
REFERENCE/POCKET NUMBER: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/09372003 GENERAL INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            84.2%;
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                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0
Matches 3; Conservative
                               TELEPHONE: 312-913-000
TELEFAX: 312-913-0002
TELEX:
                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-372-003-4
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GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Stenglen, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
VUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY: USA
ZIP: 60606
ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compactible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATE:
APPLICATION DATE: 19-701-1995
CLASSIFICATION TATA:
APPLICATION NUMBER: US/08/504,265A
FILING DATE: 19-701-1995
CLASSIFICATION NUMBER: 08/398028
FILING DATE: 03-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: KUBJARC, JGFFFCY S.
REGISTRATION NUMBER: 36,575
REGISTRATION INFORMATION:
NAME: KUBJARC, NUMBER: 36,575
REGISTRATION INFORMATION:
TELERBUCE/DOCKET NUMBER: 90936F1
TELERBUCE/DOCKET NUMBER: P0936F1
TELERBUCE/DOCKET NUMBER: P0936F1
TELERBUCE/DOCKET NUMBER: P0936F1
TELERBUCE/DOCKET NUMBER: P0936F1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
14-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: NOOMAT, KEV'IN E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 73: SEQUENCE CHARACTERISTICS:
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Best Local Similarity 75.0
Matches 3; Conservative
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1 RVRR 4
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US-09-372-003-4
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
THOUGHT: PACTT, Tech Transfer Office University of Lausanne
APPLICANT: Bonny, Christophe
TITLE OF INVENTION: INTRACLELULAR DELLUCRY OF BIOLOGICAL EFFECTORS
TILE REFERENCE: 20349-512 Transporter peptides
CURRENT APPLICATION NUMBER: US/09/977,831
CURRENT FILING DATE: 2001-10-15
FRIOR PILING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hemperead, Barbara L.
APPLICANT: Lee, Ramee
APPLICANT: Lee, Rameeh
APPLICANT: Teng, Kenneth K.
APPLICANT: Kermani, Pounch
TITLE OF INVENTION: High Affinity Ligand For p75 Neurotrophin Receptor
FILE REPRENEUE: 955-21 Sequence Nos. 1-68
CURRENT APPLICATION WIMBER: 10510/155,886
CURRENT FILING DATE: 2002-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                    Length 4;
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                                                                    Score 16; DB 19;
Pred. No. 6.4e+06;
1; Mismatches 0
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                                                                    84.2%;
75.0%;
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
                                                                  Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
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Matches 3; Conservative
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1 RVRR 4
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                          US-09-566-922C-19
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US-10-155-886-24
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US-09-566-922A-19

i Sequence 19, Application US/09566922A

i GENERAL INFORMATION:

APPLICANT: The Board of Regents of the University of Nebraska

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING IMMUNE RESPONSES MEDIATED

TITLE OF INVENTION: ANTIGEN-PRESENTING CELLS

TITLE OF INVENTION: ANTIGEN-PRESENTING CELLS

CURRENT APPLICATION NUMBER: US/09/566,922A

CURRENT PILING DATE: 1998-04-17

PRIOR PILING DATE: 1998-04-17

PRIOR APPLICATION NUMBER: US 60/005,727

PRIOR PILING DATE: 1955-10-18

PRIOR PILING DATE: 1955-10-20

NUMBER OF SEQ.ID NOS: 19

SOFTWARE: Patentin version 3.0

SEQ.ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CENERAL INFORMALION:
COMPOSITIONS AND METHODS FOR ENHANCING IMMUNE RESPONSES MEDIATED TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ENHANCING IMMUNE RESPONSES MEDIATED TITLE OF INVENTION: ANITGEN-PRESENTING CELLS
TILLE REFERENCE: UNMCS736
CURRENT APPLICATION NUMBER: US/09/566,922C
CURRENT APPLICATION NUMBER: US/09/566,922C
CURRENT FILING DATE: 1998-04-17
PRIOR FILING DATE: 1998-04-17
PRIOR FILING DATE: 1996-10-18
PRIOR FILING DATE: 1996-10-18
PRIOR FILING DATE: 1995-10-20
NUMBER: OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 19
; OTHER INFORMATION: is derivatized by a 4-methylcoumaryl-7-amide group."
US-09-372-003-20
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                                                                                     Score 16; DB 17; Length 4;
Pred. No. 6.4e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
84.2%; Score 16; DB 19; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels
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LOCATION: () ...()
OTHER INFORMATION: synthetic sequence
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US-09-566-922C-19
; Sequence 19, Application US/09566922C
; GENERAL INFORMATION:
                                                                                       84.2%;
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ORGANISM: Artificial sequence
                                                                                     Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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RVRR 4
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RVRR 4
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US-10-165-015-29
; Sequence 29, Application US/10165015
; GENERAL INFORMATION:
; APPLICANT: BACTT, Tech Transfer Office University of Lausanne
; APPLICANT: BACNT, Tech Transfer Office University of Lausanne
; APPLICANT: BOMNY, Christophe
; TITLE OF INVENTION: INTRACELLUAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 20349-512 INTRACELLUAR DELIVERY OF BIOLOGICAL EFFECTORS
; FILE REFERENCE: 2003-06-07
; PRIOR APPLICATION NUMBER: US/10/165,015
; PRIOR APPLICATION NUMBER: 60/240,315
; PRIOR APPLICATION NUMBER: 60/240,315
; PRIOR APPLICATION NUMBER: 60/240,315
; ROFTWARE: PATENTING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PATENTIN VEY: 2.1
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US-10-173-524-69
i Sequence 69, Application US/10173524
j GENERAL INFORMATION:
j APPLICANT: Komiyama, Tomoko
j APPLICANT: Fuller, Robert S.
j TITLE OF INVENTION: Eggin C Based Drugs for Treatment of Disease
j FILE REFERENCE: UM-07240
j CURRENT APPLICATION NUMBER: US/10/173,524
j CURRENT PILING DATE: 2002-06-17
j PRIOR FILING DATE: 2001-06-18
j SPRIOR FILING DATE: 2001-06-18
j NUMBER OF SEQ ID NOS: 70
j SOFTWARE: PatentIn version 3.1
j SEQ ID NO 69
LENGTH: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: TRANSPORTER; OTHER INFORMATION: PEPTIDE US-10-165-015-29
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84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels
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84.2%; Score 16; DB 27; Length 4;
Best Local Similarity 75.0%; Pred. No. 6.4e+06;
Matches 3; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Synthetic
US-10-173-524-69
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1 RVRR 4
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Search completed: June 20, 2005, 16:46:44 Job time: 330.5 secs

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1106, App

112, App

113, App

1146, App

1160, App

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112, App

1134, App

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US-10-892-402-103
US-10-892-402-106
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6: /cgn2 6/ptodata/2/paa/USO8 NEW COMB.pep:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Result No.

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Sequence 23, Application US/11051267

GENERAL INFORMATION:
APPLICANT: Lee, Se-Jin

APPLICANT: Lee, Se-Jin

APPLICANT: Lee, Se-Jin

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR RECEPTORS,
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
TITLE OF INVENTION: AGONISTS AND ANTAGONISTS THEREOF, AND METHODS OF USING SAME
TITLE OF INVENTION: 2001-02-03

PRICE PLIANG DATE: 2001-04-24

PRICE PLING DATE: 2000-07-27

PRICE APPLICATION NUMBER: 09/485,046

PRICE PLING DATE: 2000-01-31

PRICE PLING DATE: 1998-07-28

PRICE PLING DATE: 1998-01

NUMBER OF SEQ ID NOS: 29

SOFTWARE: FRAESE FRAESE FRAESE FRAESE FRAESE ANTAGONER OF SECOND OF 31

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LENGTH. A. 10 023
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APPLICANT: Li, Yuanhao
APPLICANT: Harding, Thomas
APPLICANT: Fang, Jannin
APPLICANT: Rangeh, Nagarajan
APPLICANT: Rangeh, Nagarajan
APPLICANT: Rangeh, Nagarajan
APPLICANT: Yu, De Chao
TITLE OF INVENTION: cell Specific Replication-Competent Viral Vectors Comprising
TITLE OF INVENTION: a Self Processing Peptide Cleavage Site
FILE REFERENCE: 3802-095-27
CURRENT PEPLION NUMBER: US/10/857, 498A
PRIOR APPLICATION NUMBER: US 60/475,005
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Bukaryotes
FRATURE:
NAME/KEY: SITE
LOCATION: (0)...(0)
OTHER INFORMATION: proteolytic processing site
                                                                                                                                                                                              Sequence 11, Application US/10857498A GENERAL INFORMATION:
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75.0%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
Matches 3; Conservative
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US-10-857-498A-11
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APPLICANT: Gorman, Cornelia M.
APPLICANT: Goroskreutz, Debyra J.
TITLE OF INVENTION: PROHORMONE CONVERTASE TRANSFORMED CELLS AND POLYPEPTIDE SYNTHESIS
FILLE REFERENCE: 11669.103USW3
CURRENT APPLICATION NUMBER: US 08/026,143
PRIOR APPLICATION NUMBER: US 08/026,143
PRIOR FILING DATE: 1992.03-03
PRIOR FILING DATE: 1992-12-04
PRIOR FILING DATE: 1992-05-22
PRIOR FILING DATE: 1992-05-22
PRIOR FILING DATE: 1992-05-22
PRIOR FILING DATE: 1991-05-20
PRIOR PILING DATE: 1991-05-20
PRIOR PRILOR PRIOR PRIOR PRIOR PRIOR PILING DATE: 1991-05-20
PRIOR FILING DATE: 1991-12-06
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PATCHIN VERSION 3.3
SOFTWARE: PATCHIN VERSION 3.3
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Sequence 432,
Sequence 449,
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                                                                                                                                                                                                           Sequence 110, Application US/10892402
GENERAL INFORMATION:
APPLICANT: Harris, Jennifer L.
APPLICANT: Bamciseaux, Robert
APPLICANT: Damciseaux, Robert
APPLICANT: Winssinger, Nicolas
APPLICANT: Winssinger, Nicolas
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
TITLE OF INVENTION: Thereof
TITLE OF INVENTION Thereof
FILE REFERENCE: 021288-000410US
CURRENT APPLICATION NUMBER: US 60/487,464
PRIOR APPLICATION NUMBER: US 60/487,464
PRIOR APPLICATION NUMBER: US 60/487,464
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Pred. No. 5.4e+05;
PCT-US04-26288-432
PCT-US04-26288-449
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                                                                                                   ALIGNMENTS
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 110
LENGTH: 4
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75.0%;
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Best Local Similarity 75.0%;
Matches 3; Conservative
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Best Local Similarity 75.0%
....has 3; Conservative
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; OTHER INFORMATION: Peptide
US-09-997-868A-22
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RVRR 4
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US-09-997-868A-22
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VS-09-997-868A-23

VS-09-997-868A-23

Sequence 23, Application US/09997868A

Sequence 23, Application US/09997868A

SERVERAL INFORMATION:

APPLICANT: Gorman, Cornelia M.

APPLICANT: Groskreutz, Debyra J.

TITLE OF INVENTION: FROHORMONE CONVERTASE TRANSFORMED CELLS AND POLYPEPTIDE SYNTHESIS

TITLE REFERENCE: 11669-103108W3

CURRENT APPLICATION NUMBER: US/09/997,868A

CURRENT APPLICATION NUMBER: US 00/26,143

PRIOR PILING DATE: 1993-03-01

PRIOR FILING DATE: 1993-12-04

PRIOR FILING DATE: 1992-12-06

PRIOR APPLICATION NUMBER: US 07/803,631

PRIOR PILING DATE: 1991-12-06

NUMBER OF SEQ ID NOS: 61

SOFTWARE: PatentIn version 3.3

SEQ ID NO 23
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TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
FILE REPERENCE: 02128-000410US
CURRENT FILING DATE: 2004-07-14
PRIOR APPLICATION NUMBER: US 60/487,464
PRIOR APPLICATION NUMBER: US 60/487,464
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 107
LENGTH: 4
                                                                                                                                         0; Indels
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5.4e+05;
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GENERAL INFORMATION:
APPLICANT: Harris, Jennifer L.
                                                                                        Query Match
Best Local Similarity 100.0%;
Matches 3; Conservative 0
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ORGANISM: Artificial Sequence
PEATURE:
; TYPE: PRT
; ORGANISM: Corononavirus-HKU1
US-11-129-741-2596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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ORGANISM: Artificial
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US-11-127-629-23
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                                                                                                                                                                                                                                                                                          Sequence 23, Application US/11127629

GENERAL INFORMATION:

APPLICANT: Alam, Tausif

APPLICANT: Hullett, Debra A.

APPLICANT: Sollinger, Hans W.

TITIG FOR INVERTION: Treatment of Diabetes with Synthetic Beta Cells

TITIG FOR INVERTION: Treatment of Diabetes with Synthetic Beta Cells

FILE REFERENCE: 960296.00216

CURRENT APPLICATION NUMBER: US/11/127,629

CURRENT APPLICATION NUMBER: US/213,924

PRIOR FILING DATE: 2004-08-23

PRIOR FILING DATE: 2001-11-12

PRIOR PELING DATE: 2000-03-28

PRIOR APPLICATION NUMBER: 09/537,696

PRIOR PELING DATE: 2000-03-28

PRIOR PELING DATE: 1998-07-15

PRIOR FILING DATE: 1998-07-15

PRIOR FILING DATE: 1998-07-15

PRIOR FILING DATE: 1998-07-15

NUMBER OF SEQ ID NOS: 31

SOFTWARE: PatentIn version 3.2
                                                                                             Gaps
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APPLICANT: YUEN, KWOK YUNG
APPLICANT: WOO, CHIU YAT PATRICK
APPLICANT: LAU, KAR PUI SUSANNA
APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: POON, LIT MAN
APPLICANT: POON, LIT MAN
TITLE OF INVENTION: AN NOVEL HUMAN VIRUS CAUSING RESPIRATORY TRACT
TITLE OF INVENTION: INPECTION AND USES THEREOF
FILE REPERENCE: V0690.004
CURRENT APPLICATION NUMBER: US/11/129,741
CURRENT FILING DATE: 2005-05-16
PRIOR PILING DATE: 2004-07-21
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                                         78.9%; Score 15; DB 7; Length 4; 50.0%; Pred. No. 5.4e+05; ive 2; Mismatches 0; Indels
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SOFTWARE: Patentin version 3.3
SEQ ID NO 2596
LENGTH: 4
                                         Query Match
Best Local Similarity 50.0
Matches 2; Conservative
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1 RIRR 4
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US-11-051-267-23
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US-11-127-629-23
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PRIOR PELICATION NUMBER: 09/426,282
PRIOR PELICATION NUMBER: 09/426,282
PRIOR PELICATION NUMBER: 09/668,266
PRIOR PELING DATE: 1999-10-25
PRIOR PELING DATE: 1999-10-25
PRIOR PELING DATE: 2000-09-22
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2000-11-28
PRIOR PELING DATE: 2001-05-16
PRIOR PELING DATE: 2001-10-31
PRIOR PELING DATE: 2001-12-06
PRIOR PELING DATE:
                                                                     Gaps
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APPLICANT: Carroll, Joseph M.
APPLICANT: Chun, Miyoung 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR THE REFERENCE: MPIO3-0210MNIM
CURRENT APPLICATION NUMBER: US/10/386,414A

CURRENT FILING DATE: 2003-03-11
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Pred. No. 5.4e+05;
0; Mismatches 1; Indels
h Similarity 75.0%; Pred. No. 5.4e+05; 3; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Kapeller-Libermann, Rosana
APPLICANT: Robison, Keith E.
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US-10-061-395B-43
Sequence 43, Application US/10061395B
GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/10386414A GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    White, David
Williamson, Mark W.
Cook, William James
Meyers, Rachel E.
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Similarity 75.0%;
3; Conservative
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Best Local Similarity
      Query Match
Best Local Similarity
Matches 3; Conserv
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         ; OTHER INFORMATION: rhodamine protease substrate library peptide US-10-892-402-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: rhodamine protease substrate library peptide US-10-892-402-108
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; Sequence 109, Application US/10892402
; GRNERAL INFORMATION:
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Damoiseaux, Robert
; APPLICANT: Backes, Bradley J.
; APPLICANT: IRM LLC
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Pluorogenic Enzyme Substrates and Uses
; TITLE OF INVENTION: Proceed
; TITLE OF INVENTION: Preced
; TITLE OF INVENTION: NUMBER: US 60/487,464
; PRIOR APPLICATION NUMBER: US 60/487,464
; PRIOR APPLICATION NUMBER: US 60/487,464
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: PastSEQ for Windows Version 3.0
; TENCORE IN 0.109
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APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: Backes, Bradley J.
APPLICANT: RM Lid.
TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses
TITLE OF INVENTION: Thereof
FILE REPERSOR: 021288-000410US
CURRENT APPLICATION NUMBER: US/10/892,402
CURRENT PILING DATE: 2004-07-14
PRIOR PILING DATE: 2004-07-14
NUMBER OF SEQ ID NOS: 155
NUMBER OF SEQ ID NOS: 155
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                      68.4%; Score 13; DB 6; I
75.0%; Pred. No. 5.4e+05;
tive 0; Mismatches 1;
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GENERAL INFORMATION:
APPLICANT: Harris, Jennifer L.
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                         Query Match
Best Local Similarity 75.0
Matches 3; Conservative
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US-10-892-402-109
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US-10-892-402-108
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GENERAL INFORMATION:
APPLICAMT: Kinch, Michael
TITLE OF INVENTION: EphA2, EphA4 and LMW-PTP and Methods of
TITLE OF INVENTION: Treatment of Hyperproliferative Cell Disorders
FILE REFERENCE: 10271-111-999
CURRENT APPLICATION NUMBER: 60/527,154
PRIOR APPLICATION NUMBER: 60/527,154
PRIOR APPLICATION NUMBER: 60/527,154
PRIOR APPLICATION NUMBER: 60/527,154
NUMBER OF SEQ ID NOS: 127
SOPTWARE: FastSEQ for Windows Version 4.0
## APPLICANT: Smith, Ernest S.
## TITLE OF INVENTION: Methods of Identifying Regulator Molecules
## FILE REFERENCE: 1821.0080003
## CURRENT APPLICATION NUMBER: US/10/061,395B
## CURRENT FILING DATE: 2002-02-04
## PRIOR APPLICATION NUMBER: 60/271,423
## PRIOR APPLICATION NUMBER: 60/265,880
## PRIOR PILING DATE: 2001-02-05
## PRIOR PILING DATE: 2001-02-05
## PRIOR FILING DATE: 2001-02-02
## PRIOR FILING DATE: 2001-02-02
## NUMBER OF SEQ ID NOS: 119
## SOFTWARE: Patentin version 3.1
## SECTION ON 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
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TITLE OF INVENTION: Targeted Drug Delivery Using EphA2 or
TITLE OF INVENTION: EphA4 Binding Moieties
FILE REPERENCE: 10271-120-999
FILE REPERENCE: 10271-120-999
CURRENT APPLICATION NUMBER: US/11/004,794A
CURRENT PILING DATE: 2004-12-03
PRIOR PILING DATE: 2003-12-04
PRIOR FILING DATE: 2003-12-04
SEQ ID NOS: 125
SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 75.0%; Pred. No. 5.4e+05;
Matches 3; Conservative 0; Mismatches 1;
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Pred. No. 5.4e+05;
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                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 75.0
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ORGANISM: Homo sapiens
US-11-004-794A-81
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GENERAL INFORMATION:
APPLICANT: Jessell, Thomas M.
APPLICANT: Basler, Konard
ITILE OF INVENTION: CLONING, EXPRESSION AND USES OF DORSALIN-1
FILE REFERENCE: 0575/40314-A
CURRENT APPLICATION NUMBER: US/11/107,481
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: US/10/002,278
PRIOR PLILING DATE: 2001-11-02
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Version 3.1
SEQ ID NO 17
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                                                                                                                                                     1; Indels
                                                                                                                  Length 4;
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Pred. No. 5.4e+05;
0; Mismatches 1;
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Job time : 38 secs
                                                                                                                  68.4%;
75.0%;
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Matches 3; Conservative
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Best Local Similarity 75.0
Matches 3; Conservative
; SEQ ID NO 97
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-004-795A-97
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ORGANISM: Chick
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protein search, using sw model OM protein

Run on:

June 20, 2005, 19:37:50 ; Search time 41 Seconds (without alignments) 924.620 Million cell updates/sec

2032 1 EDPQGDAAQKTDTSHHDQDH.....IEQNTKSPLFMGKVVNPTGK 394 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

alpha-1-antitrypsi alpha-1-antitrypsi alpha-1-antitrypsi alpha-1-antitrypsi alpha-1-antiprotei alpha-1-antitrypsi alpha-1-antitrypsi alpha-1-antitrypsi alpha-1-antitrypsi alpha-1-antitrypsi alpha-1-antitrypsi serine proteinase protein C inhibito contrapsin precurs contrapsin related kallistatin precur contrapsin precurs alpha-1-antiprotei alpha 1-proteinase alpha-1-antitrypsi Description SUMMARIES ITHU ITBA ITRT S60036 ITSH ITSH S21097 JX0346 S54981 IS9470 JX0154 149472 149452 JX0267 JX0267 149473 A5486 1149474 117MSC A339088 B339088 A45457 A28882 S23675 A49518 Query Match Length DB 4413 4413 4413 4413 4410 4410 4410 4410 65.0 65.0 65.0 Score Result Š.

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ITHUC B29131 A28321 A361328 A36117 A10494 S08102 S19724 A49190 A49190 A47224 S31507 S31505	150490 533415 533415 533415 740493 742440 139202 139202 139202 139202 139202 146990 566289 538066 538966 538966 538966 538966 538966 538966	A57488 A52853 A59273 A59273 OACH D74265 S70647 S7118 JC7118 JC7118 JC7118 JC7118 S19208 S19208 S1933 A35032 XHHU3	S27383 A61435 A61435 IS9611 A26423 A34761 AH1903 AH1903 AH2968 AH2968 AH2968 AH2968 AH2840 A46046 A46046 A46046 A46046
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ALIGNMENTS

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A,Note: peptides were sequenced or partially sequenced and ordered by comparison with A21 R;Weiland, K.L.; Falany, C.N.; Dooley, T.P. submitted to the RMEL Data Library, December 1989 A;Description: Identification of a cDNA encoding a variant form of the human proteolytic A;Reference number: $14476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , Molecule type: protein
, Residues: 375-409, 'L',411-413,'S' <NIE>
, Dengler, R.; Eger, G.; Lottepelch, F.; Plewan, A.; Ogilvie, A.; Emmerich, B.
iol. Chem. Hoppe-Seyler 373, 581-588, 1992
, Title: Proteolytic inactivation of alpha(1)-proteinase inhibitor in vivo: detection, cl., Reference number: $23962; MUID:92384968; PMID:1515087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 25-28;40-47;207-208;382-389;414-418 <DE2>
A; Residues: 25-28;40-47;207-208;382-389;414-418 <DE2>
A; Leicht, M.; Long, G.L.; Chandra, T.; Kurachi, K.; Kidd, V.J.; Mace, M.
Nature 297, 655-659, 1987
A; Title: Sequence homology and structural comparison between the chromosomal human alpha
A; Reference number: 139371; MUID:82220035; PMID:6979715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: Structural transition of alpha(1)-antitrypsin by a peptide sequentially similar A,Reference number: S13833; MUID:91071209; PMID:2253623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riviemann, M.A.; Narkates, A.J.; Miller, B.J. Matrix 12, 233-241, 1992. Matrix 12, 233-241, 1992. A.J. Title: Isolation and serine protease inhibitory activity of the 44-residue, C-terminal A;Reference number: S23516; MUID:93024095; PMID:1406456
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A, Molecule type: protein
A, Molecule type: protein
A, Rolecule type: protein
A, Residues: 31-385 < CHA>
R, Coutelle, C.; Speer, A.; Rogers, J.; Kalsheker, N.; Humphries, S.; Williamson, Biomed. Biochim. Acta 44, 421-431, 1985
Biomed. Biochim. Acta 44, 421-431, 1985
A; Title: Construction and partial characterization of a human liver cDNA library.
A; Reference number: 139370; WUID:85225507; PMID:3873938
                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 142-230, YY, 232-338 < WEI>
A; Cross-references: EMBL:X17122; NID:928636; PIDN:CAA34982.1; PID:928637
A; Experimental source: a variant form
R; Riley, J.H.; Bathurst, I.C.; Edbrooke, M.R.; Carrell, R.W.; Craig, R.K.
FEBS Lett. 189, 361-366, 1985
A; Fitle: Alpha-1-antitrypsin and serum albumin mRNA accumulation in normal, A; Reference number: A24013; MUID:86005469; PMID:3876243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 292-418 «RIL»
A;Cross-references: EMBL:X02920; NID:g24437; PIDN:CAA26677.1; PID:g24438
R;Schulze, A.J.; Baumann, U.; Knof, S.; Jaeger, E.; Huber, R.; Laurell, C.B.
Eur. J. Biochem. 194, 51-56, 1990
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Biochem. J. 314, 647-653, 1996
A;Title: Probing serpin reactive-loop conformations by proteolytic cleavage.
A;Reference number: S63599; MUID:96239126; PMID:8670081
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A;Accession: I39372
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A;Molecule type: DNA
A;Residues: 1-67 <LEII>
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Residues: 25-41 <SCH>
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A; Residues: 1-138, 'DG', 141-272, 'N', 274-418 <BOL>
A; Residues: 1-138, 'DG', 141-272, 'N', 274-418 <BOL>
A; Cross-references: GB:K01396; NID:928965
A; Note: this sequence has been corrected in reference A58528
A; Title: Revised sequence of full-length complementary DNA coding for human alpha-1-anti
A; Reference number: A58528; MUD:8502667; PMID:6333329
A; Contents: corrections to sequence in A90944
A; Accession: A58528
A; Molecule type: mRNA
A; Residues: 1-418 <COL
A; Residues: 1-189 <ACL
A; Residues: 1-189 <ACL
A; Residues: 1-180 <ACL
A; Residues: 1-190 <ACL
A; Residues: 1-190 <ACL
A; Residues: 1-1,13-13-140, 1985
A; NID:9177826; PIDN:CA25838.1; PID:9177827
A; Accession: A23174
A; Molecule type: mRNA
A; Residues: 1-11,13-173,'H',175-228,'D',230-418 <CIL>A; Residues: 1-11,13-173,'H',175-228,'D',230-418 <CIL>A; Residues: 1-11,13-173,'H',175-228,'D',230-418 <CIL>A; Residues: 1-11,13-140, 1985
A; Cross-references: GB:M11465; NID:9177826; PIDN:AA551546.1; PID:9177827
A; Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var A; Note: the authors state that this sequence corresponds to the M (normal) allele; 3 var A; Note: the authors date and variation of human alpha-1-antitrypsin.
A; Accession: A329-334 y 1982
A; Archerican: A339-314 WUID:82220135; PMID:7045697
A; Accession: A328-34
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A; Title: The identification of epitopic sites in human alpha-1-proteinase inhibitor. A; Reference number: A32336; MUID:88049621; PMID:2445337
A; Accession: A32336
A; Molecule type: protein
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A;Residues: 1-124,'H',126-325,'I',327-418 <ROS>
A;Cross-references: EMBL:X01683; NID:928965
R;Bollen, A.; Herzog, A.; Cravador, A.; Herion, P.; Chuchana, P.; Vander Straten, A.; Lq
                                                                                                                                                                                                                                NiAlternate names: alpha-1-AT; alpha-1-proteinase inhibitor
Cispecies: Homo sapiens (man)
Cibate: 30-Nov-1980 #sequence revision 31-Mar-1992 #text_change 09-Jul-2004
CiAccession: A21853; B21853; A33352; A90944; A58528; A23174; A9281; A32336; S14476; A24
R;Long, G.L.; Chandra, T.; Woo, S.L.C.; Davie, E.W.; Kurachi, K.
Bicchemistry 23, 4828-4837, 1984
A;Title: Complete sequence of the CDNA for human alpha-1-antitrypsin and the gene for th
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A; Residues: 1-287, 'V', 289-418 <LON2>
A; Cross-rectar locates: GB: KO2212; NID: g177830; PIDN: AABS 9495.1; PID: g177831
A; Experimental source: S variant allele
B; Rosenberg, S.; Barr, P.J.; Najarian, R.C.; Hallewell, R.A.
Rivure 312, 77-80, 1984
A; Title: Synthesis in yeast of a functional oxidation-resistant mutant of human alpha-1-
A; Reference number: A93352; MUID: 8503645; PMID: 6387509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA 2, 255-264, 1983
A;Title: Cloning and expression in Escherichia coli of full-length complementary DNA cod
A;Reference number: A90944; MUID:84107980; PMID:6319097
A;Accession: A90944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-418 <LON1>
A;Cross-references: UNIPROT:P01009; GB:K02212; NID:g177830
A;Experimental source: M (normal) allele
A;Accession: B21853
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316 TVLGHLGITKVFSNGADLSGVTEDAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 387-399, D', 401-418 <COU>
A;Cross-referencés: GB:MZ6123; NID:g177815; PIDN:AAA51545.1; PID:g177816
B;Faber, J. D.; Wridinger, S.; Oldk, K.
Am. J. Hum. Genet. 46, 1158-1162, 1990
A;Title: Sequence data of the rare deficient alpha-1-antitrypsin variant PI Zaugsburg.
A;Reference number: A35338; MUID:90252805; PMID:2339709
A;Reference number: A2674; PL26-128;363-365, K', 367-369 <FAB>
A;Reference number: Multh Lya-566 arose from the M2 variant with His-125
A;Reference number: A50775; PDB:AFAI
A;Contents: annotation; X-ray crystallography, 3.0 angstroms, tetragonal form 1, residue A;Reference number: A50774; PDB:ARI
A;Contents: annotation; X-ray crystallography, 3.1 angstroms, hexagonal form, residue B;Rochaven Protein Data Bank, September 1988
A;Reference number: A50774; PDB:BAPI
B;Contents: annotation; X-ray crystallography, 3.1 angstroms, tetragonal form, residue R;Cochermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
B;Cochermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
B;Lochermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
B;Lochermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
B;Lochermann, H.; Tokuoka, R.; Deisenhofer, J.; Huber, R.
B;Hochermann, H.; Dokuoka, R.; Deisenhofer, J.; Huber, R.
B;Hochermann, H.; Dokuoka, R.; Deisenhofer, J.;
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A, Gene: GDB:PI
A, Introns: 216/1; 306/2; 355/3
A, Note: it also inhibits plasmin, thrombin, kallikrein, trypsin, and chymotrypsin
C; Buperfamily: Serpin
C; Superfamily: Ser
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A;Contents: annotation; X-ray crystallography, 3.0 angstroms
A;Contents: annotation; X-ray crystallography, 3.0 angstroms
R;Carrell, R.W.; 301-303, 1081
A;Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A;Title: Human alpha-1-antitrypsin: carbohydrate attachment and sequence homology.
A;Reference number: A58526; MUD:82095611; PMID:6976274
A;Contents: annotation; carbohydrate attchment sites
C;Comment: The Z variant allele has Lys-366. Deficiency of the normal inhibitor in indivasis.
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Pred. No. 2.8e-131;
3; Mismatches 3; Indels (
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Best Local Similarity 98.5%;
Matches 388; Conservative
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CiAccession: A01248
Rivacchi, K.; Chandra, T.; Degen, S.J.F.; White, T.T.; Marchioro, T.L.; Woo, S.L.C.; Dav Proc. Natl. Acad. Sci. U.S.A. 78, 6826-6830, 1981
A;Title: Cloning and sequence of CDNA coding for alpha-1-antitrypsin.
A;Reference number: A01248; MUID:82082539; PMID:7031661
A;Accession: A01248
A;Molecule type: mRNA
A;Molec
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LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
                                                                                           265 IMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 324
                                                                                                                                                                                                                                                                                                                                         325 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Papio sp. (baboon)
C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 15-Sep-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 EDPQGDAAQKTDTPPHDQNHPTLNKITPSLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-1-antitrypsin precursor - baboon (fragment) N;Alternate names: alpha-1-proteinase inhibitor C;Species: Papio sp. (baboon)
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375

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A;Cross-references: UNIPROT: P97277; EMBL: D49709; NID:g1088432; PIDN: BAA08557.1; PID:g1794
A;Note: the source is designated as Syrian hamster
C;Superfamily: Serpin
F;1.24|Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antitrypsin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encoding plasma alpha-1-antiprot
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Ribrown, W.M.; Dziegielewska, K.M.; Foreman, R.C.; Saunders, N.R.; Wu, Y.
Nucleic Acids Res. 17, 6398, 1989
A;Title: Nucleotide and deduced amino acid sequence of sheep alpha-1 antitrypsin.
A;Reference number: S05312; MUD:89366677; PMID:2788872
A;Accession: S05312
A;Accession: S05312
A;Molecule type: mRNA
A;Residues: 1-416 < MRNA
A;Cross-references: UNIPROT:P12725; EMBL:X15555; NID:91369; PIDN:CAA33561.1; PID:91370
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                                                                                                                                                                                                       alpha-1-antitrypsin precursor - golden hamster
N;Alternate names: alpha-1-antiproteinase
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accesaion: S60036
R;Nakatani, T.; Suzuki, Y.; Yoshida, K.; Sinohara, H.
Biochim: Biophys. Acta 1283, 245-248, 1995
A;Accesaion: S60036
A;Title: Molecular cloning and sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoding plasma algable and the sequence analysis of cDNA encoderation and the sequence analysis of cDNA encodera
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 AQKTDISHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 IFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.4%; Score 1431.5; DB 270.2%; Pred. No. 1.1e-91; tive 55; Mismatches 59;
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387 SPFIAIIYDRQTAKSPLFVGKVVDPT 412
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386 HPFIFMIVESETQSPLFVGKVIDPT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alpha-1-antitrypsin precursor - sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 70.29
Matches 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: mRNA
A;Residues: 4-411 <CHA>
A;Cross-references: UNIPROT:P17475; GB:M32247; NID:g203062; PIDN:AAA40788.1; PID:g203063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA ** A; Molecule type: mRNA ** A; Molecule type: mRNA ** A; Molecule type: 188-246, 11, 248-321, 10, 323-389 <** FLI> ** A; Kesidues: 188-246, 11, 248-321, ND: G57299; PIDN: CAA34349.1; PID: g930263 ** A; Crosss-references: EMBL: X16273; NID: g57299; PIDN: CAA34349.1; PID: g930263 ** R; Misumi, Y.; Sohda, M.; Ohkubo, K.; Takami, N.; Oda, K.; Ikehara, Y. A. Biochem. 108, 230-234, 1990 ** A; Title: Molecular cloning and sequencing of the CDNA of rat alpha-1-protease inhibitor A; Reference number: JX0123; MUID: 91035351; PMID: 2229024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primary target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      266 ATAIFLLPDDGKMQHLEQTLTKDLISRFLLNRQTRSAILYFPKLSISGTYNLKTLLSSLG 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAIFFLEDEGKLOHLENELTHDIITKFLENEDRRSASIHLPKLSITGTYDLKSVLGOLG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 ITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVKFN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 TKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 SKGDTRKQILEGLEFNLTQIPEADIHKAFHHLLQTLNRPDSELQLNTGNGLFVNKNLKLV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
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       alpha-1-antitrypsin precursor - rat
N;Alternate names: alpha-1-proteinase inhibitor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Mar-1992 #sequence ravision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A33892; B3382; 508016; JX0123; A38823
R;Chao, S.; Chai, K.x.; Chao, L.; Chao, J.
Biochemistry 29, 323-329, 1990
A;Title: Molecular cloning and primary structure of rat alpha-1-antitrypsin.
A;Reference number: A33892; MUID:90148955; PMID:2302382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188 IFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMPNIQHCKKLSSWVLLMKYLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor F;1-24/Domain: signal sequence #status predicted <SIG> F;2-411/Product: alpha-1-antitrypsin #status experimental <MAT> F;5-411/101.265/Binding site: carbohydrate (Asn) (covalent) #status predicted F;376/Inhibitory site: Met (elastase, collagenase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-13, G',15-83, V',85-247, Y',249-317, N',319-411 <MIS>
A; Cross-references: GB: D00675; NID: g220648; PIDN: BAA00579.1; PID: g220649
A; Experimental source: serum
A; Accession: A38823
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69.9%; Pred. No. 1.6e-92;
:ive 62; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Accession: B33892
A,Molecule type: protein
A,Residues: 25-57 <CH2>
R,Flink, I.L.; Bailey, T.; Morkin, E.
submitted to the EMBL Data Library, August 1989
A,Reference number: S08016
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Matches 269; Conservative
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A,Title: Plasma alpha-1-antiproteinase from the Mongolian gerbil, Meriones unguiculatus:
A,Reference number: JX0346, MUID:95155268; PMID:7852275
                                                                                                                                                                                                                                                                           86 LSLGAKGNTHTEILKGLGFNLTELAEAEIHKGFQHLLHTLNQPNHQLQLTTGNGLFINES 145
                                                                                                                                                                                                                                                                                                                                                                                                         146 AKLVDTFLEDVKNLYHSEAFSINFRDAEBAKKKINDYVEKGSHGKIVELVKVLDPNTVFA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 LVNYISFKGKWEKPFEMKHTTERDFHVDEQTTVKVFWMNRLGMFDLHYCDKLASWVLLLD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            326 GDVGITEVFSDRADLSGITXEQPLKVSKALHKAALTIDEKGTEAVGSTFLEAIPMSLPPD 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 LVNYIPPKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 YLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    304 GOLGITKVFSNGADLSGVTERAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha-1-antiproteinase precursor - Mongolian jird
C;Species: Meriones unguiculatus (Mongolian jird)
C;Date: 22-Apr-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: JX0346; PC2357
R;Goto, K.; Suzuki, Y.; Yoshida, K.; Yamamoto, K.; Sinohara, H.
                                                                                                                                         28 QGHAVQETDDTSHQE--AACHKIAPNLANFAFSIYHHLAHQSNTSNIFFSPVSIASAFAM
                                                                                                                                                                                                                                        64 LSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQG
                                                                                                                                                                                                                                                                                                                                                                          124 LKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFA
                                                                                                  4 QGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAM
Pred. No. 4e-90;
61; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 VKFNKPFVFLMIEQNTKSPLFMGKVVNPT 392
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                                   266; Conservative
   Similarity
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NyAlternate names: alpha-1-proteinase inhibitor; proteinase inhibitor Inh3
Cispeciaes: Bos pringenius taurus (cattle)
Cispeciaes: Bos pringenius taurus (cattle)
CyAccession: $21097; PC2040; $18920
CyAccession: $21097; PC2040; $18920
CyAccession: $21097; PC2040; $18920
A;Sinha, D.; Bakhshi, M.R.; Kirby, E.P.
Biochim. Biophys. Acta 1130, 209-212, 1992
A;Title: Complete cDNA sequence of bovine alphal-antitrypsin.
A;Reference number: $21097; MUID:92223096; PMID:1562597
A;References: UNIPROT:P34955; EMBL:X63129; NID:941; PIDN:CAA44840.1; PID:942
A;Cross-references: UNIPROT:P34955; EMBL:X63129; NID:941; PIDN:CAA44840.1; PID:942
A;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 209-Thr
B;Sinha, D.; Yang, X.; Emig, F.; Kirby, E.P.
                                      primary target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 LSLGAKGNTHTEILEGLGFNLTELAEAEIHKGFQHLLHTLNQPNHQLQLTTGNGLFINES 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 AKLVDTFLEDVKNLHHSKAFSINFRDAEBAKKKINDYVEKGSHGKIVDLVKDLDQDTVFA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 LVNYISFKGKWEKPFEVEHTTERDFHVNEQTTVKVPMANRLGMFDLHYCDKLASWVLLLD 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  266 YVGNVTACFILPDLGKLQQLEDKLANBLLAKFLEKKYASSANLHLPKLSISETYDLKTVL 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 LKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVNYI PPKGKWERPPEVKDTEEEDPHVDQVTTVKVPMMKRLGMFNI OHCKKLSSWVLLMK 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 YLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVL 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 GQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28 OGHAVOETDDTAHOE--AACHKIAPNLANFAFSIYHKLAHOSNTSNIFFSPVSIASAFAM
                                                           psin.
C;Superfamily: Serpin
C;Superfamily: serpin
C;Superfamily: serpin
C;Superde: acute phase; glycoprotein; plasma; serine proteinase inhibitor
C;Keywords: acute phase; glycoprotein; predicted <81G>
E;1-24,Domain: signal sequence #status predicted <81G>
E;25-416/Product: alpha-1-antitrypsin #status predicted <WAT>
F;85-416/Product: alpha-1-antitrypsin #status predicted
F;88,105,269/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;380/Inhibitory site: Met (elastase, collagenase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Molecule type: 5-44 cs12>
C; Superfamily: Serpin
C; Keywords: acute phase; glycoprotein; plasma; serine proteinase inhibitor
F;1-24/Domain: signal sequence #status predicted cs1G>
F;25-416/Product: alpha 1-antitrypsin #status predicted cMAT>
F;68,105,143,269/Binding site: carbohydrate (Asn) (covalent) #status predic
A,Note: the authors translated the codon ATC for residue 195 as Ala
C,Comment: Alpha-1-antitrypsin is an inhibitor of serine proteinases. Its
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |:||:||:||:||
386 VEPNRPFLCILYDRNTKSPLFVGKVVNPT 414
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A/Accession: UX0346
A/Accession: UX0346
A/Rolecule type: mRNA
A/Rossidues: 1-406 <GOT>
A/Rolecule type: protein
A/Accession: PC2357
A/Rolecule type: protein
C/Superfamily: Serpin
C/Superfamily: Serpin
F/1-24/Domain: signal sequence #status predicted <SIG>
F/155-406/Product: alpha-1-antiproteinase #status predicted <MAT>
F/383-387/Region: serpin binding #status predicted (Asn) (covalent) #status predicted
F/59,96,134,260,403/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/311/Inhibitory site: Met (trypsin, chymotrypsin, elastase) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68 TKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 DKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNY
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61; Indels
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69.3%; Score 1409; DB 2; Length 416;

Query Match

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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 09-Jul-2004
N;Saito, A; Sinohara, H.
J. Biochem. 109, 158-162, 1991
A;Title: Cloning and sequencing of cDNA coding for rabbit alpha-1-antiproteinase F: aminc A;Reference number: JX0154; MuID:91201273; PMID:2016265
A;Accession: JX0154
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 QETDTSQKDQS-PASHEIATNLGDFAISLYRELVHQSNTSNIFFSPVSIATAFAMLSLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 KFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 KFLEEAKNHYQAEVFSVNFAESEEAKKVINDFVEKGTQGKIAEAVKKLDQDTVFALANYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 FFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKXLSSWVLLMKYLGNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 OKTDISHHDODHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGT
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64.1%; Pred. No. 1.9e-84;
ive 70; Mismatches 67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 KPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 64.1
Matches 248; Conservative
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S54981
alpha-1-antiproteinase isoform E precursor - rabbit
C; Species: Oryctolagus cuniculus (domestic rabbit)
C; Bate: 28-Oct-1956 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C; Accession: S24981; S72199
R; Saito, A.; Sinohara, H.
Biochem. J. 307, 369-375, 1995
A;Title: Rabbit alpha-1-antiproteinase E: a novel recombinant serpin which does not inhit A; Reference number: S54981; WUD: 95251597; PMID: 7733871
A; Rocession: S54981
A; Rocession: S54981
A; Rocession: S54981
A; Rocession: S72199
A; Rolecule type: mRNA
A; Residues: 1-413 < SAI1>
A; Rocession: S72199
A; Rolecule type: protein
A; Residues: 25-33;374-387 < SAI2>
C; Superfamily: Serpin
C; Keywords: acute phase; emphysema; glycoprotein; plasma; serine proteinase inhibitor
F; 1-24/Domain: signal sequence #status predicted <SIG>F; 25-413/Product: alpha-1-antiproteinase E #status experimental <WAT>
                                                                                                                                           245
     247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 LOHKFLEDAKNLYQSEAFLVDFRDPEQAKTKINSHVEKGTRGKIVDLVQELDARTLLALV 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 NYVFFKGKWEKPFEPENTKEEDFHVDATTTVRVPMASRLGMYVMFHCSTLASTVLRMDYK 264
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                                                                                                                                                                                                                    ITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVKFN 367
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                               NY I FFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNI QHCKKLSSWVLLMKYL
  I FFKGKWERPFEVKOTEEEDFHVDQVTTVKVPMMKRLGMPNIQHCKKLSSWVLLMKYLGN
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LDRPFLFVIYSHEIKSPLFVGKVVDPT 411
                                                                                                                                                                                                                                                                                                                           KPFVFLMIEQNTKSPLFMGKVVNPT 392
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C;Accession: 149472
R;Borriello, F.; Krauter, K.S.
R;Borriello, F.; Krauter, K.S.
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary diversive and A;Reference number: 149470; MUD: 92052104; PMID: 1946354
A;Accession: 149472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q00896; GB:M75720; NID:g191845; PIDN:AAC28868.1; PID:g191846
C;Genetics:
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                                                                       308
                                                                                                                                                            316 TRIFNNGADLSGITEENAPLKLSKAVHKAVLTIDETGTEAAAATVFEAVPMSMPPILRFD 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        309 TKVFSNGADLSGVTEE-APLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVKFN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
                                                                                                                                                                                                                                                                                                                                   alpha-1 proteinase inhibitor 3 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 LFKGKWKKPFDPENTERAEFHVDKSTTVKVPMMLSGMLDVHHCSILSSWVLLMDYAGNA
                                                                                        28 QETDISQKDQS-PASHEIATNLGDFAISLYRELVHQSNIFFSPVSIATAFAMLSLGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 LFKGKWKKPFDPENTERAEFHVDESTTVKVPMMTLSGMLDVHHCSTLSSWVLLMDYAGNA
   FFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNA
                                                                       TAIFFLPDEGKLOHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 QKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 FFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-413 <RES>
                                                                                                                                                                                                                                  368 KPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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C;Species: Mus musculus (house mouse)
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C;Superfamily: Serpin
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Best Local S
Matches 249
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c;Species: Mus musculus (house mouse)
C;Accession: 149411
R;Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary dive A;Reference number: 149470; MulD:92052104; PMID:1946354
A;Accession: 149471
A;Accession: I49471
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Accession: L402 <RES>
A;Residues: 1-402 <RES>
A;Cross-references: UNIPROT:P22599; GB:M75716; NID:g191843; PIDN:AAC28865.1; PID:g191844
C;Genetics: alpha-1 PI-2
C;Superfamily: Serpin
A;Molecule type: mRNA
A;Rosidues: 1-413 <SAI>
A;Cross-references: UNIPROT:P23035; GB:X57710; NID:g1455; PIDN:CAA40881.1; PID:g1456
C;Superfamily: Serpin
                                                                                                                                                                                                                                                                                                                                                                        NYIFFKGKWERPFEVKOTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYL 245
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64.1%; Pred. No. 4.7e-84;
ive 69; Mismatches 68;
                                                                                      65.1%; Score 1322; DB 2; 64.3%; Pred. No. 4.2e-84;
                                                                                                                         63; Mismatches
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                                                                                                     Similarity 64.3
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Best Local Similarity 64.1<sup>3</sup>
Matches 248; Conservative
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Matches 249;
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                                                                                      Query Match
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C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: 149452
R;Sifers R.N.; Lediley, F.D.; Reed-Fourquet, L.; Ledbetter, D.H.; Ledbetter, S.A.; Woo, Genomics 6, 100-104, 1990
A;Title: Complete cDNA sequence and chromosomal localization of mouse alpha-1-antitrypsi A;Accession: 149452, MUID:90152670; PMID:2303252
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residuae: 1-413 cRES-
A;Cross-references: UNIPROT:P22599; GB:M25529; NID:g191549; PIDN:AAA37132.1; PID:g309079
C;Superfamily: Serpin
                                                                                                                                                                                                                                                                                                                          128
                                                                                                                                                                                                                                                                                                                                            129 KFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNYI 188
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                                                                                                                                                                                                 65.0%; Score 1320; DB 2;
64.1%; Pred. No. 5.8e-84;
ive 69; Mismatches 68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368 KPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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Best Local Similarity 64.1*
Matches 248; Conservative
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ALEBULT 14

JY0267

alpha-1-antiproteinase S-1 precursor - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: 100267
C;Accession: 113, 456-461, 1993
A;Title: Rabbit plasma alpha-1-antiproteinase s-1: cloning, sequencing, expression, and A;Reference number: JX0267; MUID:93293795; PMID:8514734
A;Accession: JX0267
A;Ross-references: UNIPROT:Q07298; GB:D16104; NID:g286191; PIDN:BAA03678.1; PID:g303762
A;Ross-references: UNIPROT:Q07298; GB:D16104; NID:g286191; PIDN:BAA03678.1; PID:g303762
A;Ross-references: UNIPROT:Q1998; GB:D16104; Albit mature protein, was confix
C;Roywords: glycoprotein
C;Roywords: glycoprotein
C;Roywords: glycoprotein
C;Roywords: glycoprotein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-413/Product: alpha-1-antiproteinase S-1 #status experimental <MAT>
F;65,102,266/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Length 413;

; Score 1315; DB 2; ; Pred. No. 1.3e-83; 59; Mismatches 77;

64.7%;

Best Local Similarity 64.99 Matches 251; Conservative 65

DAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLS

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C;Accession: I49473
R;Borriello, F.; Krauter, K.S.
Proc. Natl. Acad. Sci. U.S.A. 88, 9417-9421, 1991
A;Title: Multiple murine alpha 1-protease inhibitor genes show unusual evolutionary diversion: I49470; MUID:92052104; PMID:1946354
A;Reference number: I494773
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-413 <RES>
A;Cross-references: UNIPROT:Q00897; GB:M75718; NID:g191847; PIDN:AAC28867.1; PID:g191848
C;Genetics:
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                                                                                                                                                                                                                                       GNATALFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQ 305
                                                                                                                                                                                                                                                                                                                        LGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVK 365
                                                                               126 LVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFALV 185
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                    84
                                                                                                                                                            alpha-1 proteinase inhibitor 4 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
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28 QETDTSQXDQS-PASHBIATNLGDFALRLYRELVHQSNTSNIFFSPVSIATAFAMLSLGS
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; Pred. No. 2.8e-83;
68; Mismatches 70;
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Best Local Similarity 63.8%;
Matches 247; Conservative 66
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A;Gene: alpha-1 PI-4
C;Superfamily: Serpin
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OM protein - protein search, using sw model

Run on:

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Title: Perfect score: Sequence:

PDX1 2032 1 EDPQGDAAQKTDTSHHDQDH.....IEQNTKSPLFMGKVVNPTGK 394

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 seqs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 100 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

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TISSUE=Fetal liver;
Zhang C., Yu Y., Zhang S., Ouyang S., Luo L., Wei H., Zhou G.,
Zhou W., Bi J., Zhang Y., Liu M., He F.;
"Functional prediction of the coding sequences of 32 new genes deduced
by analysis of cDNA clones from human fetal liver.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nukiwa T., Satoh K., Brantly M.L., Ogushi F., Fells G.A., Courtney M.,
                               AlAT HUMAN STANDARU;
POLOG9; Q13672; Q56E89; Q56E81; Q5PLP0;
21-JUL-1986 (Rel. 01, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (RRO0664-RRO2209)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-85176977; PubMed-2985281;
Ciliberto G., Dente L., Cortese R.;
"Cell-specific expression of a transfected human alpha 1-antitrypsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Long G.L., Chandra T., Woo S.L.C., Davie E.W., Kurachi K.;
"Complete sequence of the cDNA for human alpha 1-antitrypsin and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGUENCE FROM N.A.
TISSUB=Colon, and Ovary;
MEDLINE=22388257, PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenberg S., Barr P.J., Najarian R.C., Hallewell R.A., "Synthesis in yeast of a functional oxidation-resistant mutant of
                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                            GEOURNCE FROM N.A.

MEDLINE=84107980; PubMed=6319097;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=85047190; PubMed=6093867;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=85036645; PubMed=6387509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene for the S variant.";
Biochemistry 23:4828-4837(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human alpha-antitrypsin.";
Nature 312:77-80(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 41:531-540(1985)
                                                                                                                                                                                     Homo sapiens (Human)
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RESULT 1
                                     AAAAKKGAKKIIBAAKGAKIIBAKAAKKAAKIIBAKKAKAKKIKIAAKKAKKKKIKIKAKKAKKAKKAKKAKAKAKA
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McBwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., A. Villalon D.K., Muzuy D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., A. Rodriguez A.C., Grimwood J., Schwutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A. Schnerch A., Schein J.B., Jones S.J., Marra M.A., MEDLINE=22660472; PubMed=12754519; DOI: 10.1038/nbt827; Zhang H., Li X.-J., Martin D.B., Abbersold R.; Interview of quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry."; Nat. Biotechnol. 21:660-666(2003). Carrell R.W., Jeppsson J.-O., Laurell C.-B., Brennan S.O., Owen M.C., Vaughan L., Boswell D.R.; "Structure and variation of human alpha 1-antitrypsin."; Nature 298:329-334(1982). MEDLINE-82220035; PubMed-6979715;
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PRELIMINARY SEQUENCE OF 25-418. Proc. 41:1016-1016(1982). and mouse cDNA sequences." SEQUENCE OF 25-418. Williamson R.; Chan S.K.;

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Sinohara
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NON TER
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                                                                                                                                                                         361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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"Revised sequence of full-length complementary
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                                                                                                                                                                                                                                                                                                                                                                                       Cercopithecinae; Cercopithecus.
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                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
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DNA 3:327-330(1984).
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TISSUE=Kidney;
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01-JUL-1997
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                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=20386623; PubMed=10933492;
Blliott P.R., Pei X.Y., Dafforn T.R., Lomas D.A.;
Blliott P. R. of a 2.0 A structure of alphal-antitrypsin reveals targets for rational drug deeign to prevent conformational disease.";
Protein Sci. 9:1274-1281(2000).
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MEDLINE-91241132; PubMed=2035534;
Okayama H., Brantly M., Holmes M., Crystal R.G.;
"Characterization of the molecular basis of the alpha 1-antitrypsin allele.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                      1
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"Alpha 1-antitrypsin: structure, function and molecular biology
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MEDLINE=88324438; PubMed=2901226;
Nukiwa T., Brantly M.L., Ogushi F., Fells G.A., Crystal R.G.;
"Characterization of the gene and protein of the common alpha antitrypsin normal M2 allele.";
Am. J. Hum. Genet. 43:322-330(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Characterisation of the alpha-1-antitrypsin M3 gene, a normal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT M3 ASP-400.
MEDLINE=90368097; PubMed=2394452;
Graham A., Hayes K., Weidinger S., Newton C.R., Markham A.P.,
                                                                                                                                                                                                                                                                                                                                          Wu Y., Foreman R.C.; "The molecular genetics of alpha 1 antitrypsin deficiency."; Bioessays 13:163-169(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 418;
                                    Engh R., Loebermann H., Schneider M., Wiegand G., Huber R.,
Laurell C.-B.;
Tripe S variant of human alpha 1-antitrypsin, structure and
implications for function and metabolism.";
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Pred. No. 3.5e-125;
3; Mismatches 3;
            X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) MEDLINE-89221004; PubMed=2785270;
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WARLINE=89154435; PubMed=2784123; MEDLINE=89154435; PubMed=2784123;
                                                                                                                                                                                                                             MEDLINE=89352843; PubMed=2669992;
                                                                                                                                                                                                                                                                                                                            MEDLINE=91315455; PubMed=1859394;
                                                                                         Protein Eng. 2:407-415(1989).
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240
                                205 VFALVNYIPPKGKWERPFEVKDTEBEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLLSSWVL 264
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                                                                                                                                                                                                                                                                       301 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI 360
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                                                                                                                                                                                                                                                                                                               325 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI
                                                                                                                                     241 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK
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Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Alpha-1-antitrypsin (Fragment)
Cercopithecus aethiops (Green monkey) (Grivet).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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359; Conservative
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TISSUE=Fetal liver;
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VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
                              LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
                                                                                                                                                       243 IMKYLGNATAIFFLPDEGKLOHLENELTHDIIITKFLENENRRSANLHLPKLAITGTYDLK 302
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Pfam; PF00079; Serpin; 1.
SMART; SMORD93; SERPIN; 1.
ACUTE PROSITE; PS00284; SERPIN; 1.
Acute phase; Glycoprotein; Plasma; Serine protease inhibitor; Serpin;
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21-JUL-1986 (Rel. 01, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
41pha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (AAT) (Fragment).
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MEDILINE=82082539; PubMed=7031661;

MEDILINE=82082539; PubMed=7031661;

Kurachi K., Chandra T., Friezner Degen S.J., White T.T.,

Marchiloro T.L., Woo S.L.C., Davie B.W.;

"Cloning and sequence of cDNA coding for alpha 1-antitrypsin.";

Proc., Natl. Acad. Sci. U.S.A. 78:6826-6830(1981).

-!- FUNCTION: Inhibitor of serine protesses. Its primary target is elastage, but it also has a moderate affinity for plasmin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name-SERPINA1; Synonyms-PI;
Papio anubis (Olive baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                                                                                                                                                                                                                                                                                                                                                         PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY: Plasma.
-!- SIMILARITY: Belongs to the serpin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reactive bond
N-linked (Glc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-linked
N-linked
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; J00321; AAA35377.1; -. HSSP; P01009; 1EZX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Papio.
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P01010;
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SEQUENCE
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                                                                                                                                                                                             76 PAMLSLGTKADTHSEILEGLNFWLTEIPEAQVHEGFQELLRTINKPDSQLQLTTGNGLFL 135
                                                                                                                                                                                                                                                                180
                                                                                                                                                                                                                                                                                                                                                                                     196 VFALVNYIFFKGKWERPFEVEATEEEDFHVDQATTVKVPMMRRLGMFNIYHCEKLSSWVL 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               316 TVLGHLGITKVFSNGADLSGVTEDAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI 375
                                                                                                                                                                                                                                                                                                                                                          181 VPALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
                                                                                                                75
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                                                                                            16 EDPQGDAAQKTDTPPHDQNHPTLNKITPSLAEPAFSLYRQLAHQSNSTNIFFSPVSIATA
                                                                                                                                                                                                                                                                121 SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
                                                                                                                                                                                                                                                                                         301 SVLGQLGITKVPSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI
                                                                     EDPQGDAAQKTDTSHHDQDHPTFNK1TPNLAEFAFSLYRQLAHQSNSTN1FFSPVS1ATA
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                      Gaps
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CS0DM003YH14 of Fetal liver of Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                      Indels
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Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protease inhibitor; Serine protease inhibitor; Serpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1701; DB 2; 1
Pred. No. 3.8e-105;
3; Mismatches 0;
                        14;
91.1%; Pred. No. 2.5e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 PPEVKENKPFVFLMIEQNTKSPLFIGKVVNPTQK 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                      21; Mismatches
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01-JUN-2003 (TEMBLrel. 24, Last seg
01-MAR-2004 (TEEMBLrel. 26, Last ann
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99.1%;
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412 AA;
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SEQUENCE
                     Query Match
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                   215
                                                                                                           VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 275
                                                                                                                                                        SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180
                                                                                               VPALVNYIPPKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
                                                                                                                                           LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
                                                                Acute phase; Glycoprotein; Plasma; Serine protease inhibitor; Serpin; Signal.

SIGNAL 1 24 Potential.
                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor).
Callosciurus caniceps (Gray-bellied squirrel).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-1-antiproteinase.
Reactive bond (By similarity).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
N-linked (GlCNAc. .) (Potential).
                                                                                                                                                                                                  SVLGQLGITKVFSNGADLSGVTEEAPLKLSK 331
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HSSP; P01009; 1QMB.
InterPro; IPR000215; Prot_inh_serpin.
                                                                                                                                                                                                                                                                                        28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                   STANDARD;
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378
378
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A1AT CALCN
054763;
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SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324 TLGITKVFSNEADLSGVTEEAPLKLSKGVHKAVLTIDERGTEAAGVTVLEAIPMSLPPDV 383
                                                                                                                                                                                                                                                                                                                                                                         125 KLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVBKGTQGKIVDLVKBLDRDTVFAL 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLG 304
                                                                                                                                                                                                             83
                                                                                                                                                           64
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                                                                                                                                                                                       25 GD-AQETDASKDDHEHPACHKIAPNLAEFAFDLYRVLARQSNTTNIFFSPVSVATALAAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 OLGITKVPSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEV
                                                                                                                                                        5 GDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNYIFFKCKWERPFEVKDTEEBDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKY
                                                                                                      Gaps
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InterPro; IRF000015; Prot_inh_serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
Protease inhibitor; Serine protease inhibitor; Serpin.
NON TER
SEQÜENCE 309 AA; 35116 MW; SAF00026C06FBE9B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Full-length cDNA clone CSODM003YH10 of Fetal liver of Homo sapiens (human) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                  DB 1; Length 412;
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                                                                                                      59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the serpin family.
EMBL; BX248002; CAD62334.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li W.B., Gruber C., Jessee J., Polayes D.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
45729 MW; 7235668E9EE8FCC6 CRC64;
                                               72.5%; Score 1472.5; DB 72.7%; Pred. No. 7.2e-90; tive 46; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       365 KFNKPFVFLMIEQNTKSPLFMGKVVNPT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   384 RFDRPFLIIIYEHYTKSPLFVGKVVNPT 411
                                                                                                      Matches 282; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 279; Conservative
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TISSUE=Fetal liver;
Li W.B., Gruber C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Fetal liver;
                                                                             Local Similarity
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Best Local Similarity
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                           Matches
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                                                                                               61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120
                                                                                                                              PAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 147
                                                                                                                                                                                             121 SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180
                                                                                                                                                                                                                                                                                          VFALVNYIPPKCKWERPPEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
                                                                                                                                                                                                                                                                                                                           208 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 267
                                               87
                              EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
                                                                                                                                                                                                                           EDPOGDAAOKTDTSHHDODHPTFNK1TPNLAEFAFSLYROLAHOSNSTN1FFSPVS1ATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Alpha-1-antitrypsin precursor (Alpha-1 protease inhibitor) (Alpha-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Portine alpha-1-antitrypsin (PI): cDNA sequence, polymorphism and assignment to chromosome 7q2.4-q2.6."; Anim. Genet. 27.85-89(1996).
-!- FUNCTION: Inhibitor of serine proteases. Its primary target is elastase, but it also has a moderate affinity for plasmin and thrombin (By similarity).
-!- SUBCELLULAR LOCATION: Extracellular.
-!- SIMILARITY: Belongs to the serpin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archibald A.L., Couperwhite S., Mellink C.H.M., Lahbib-Mansais Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protease inhibitor; Serpin; Signal
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N-linked (GlCNAc. . .) (Potential)
N-linked (GlCNAc. . .) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                    268 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRR 309
                                                                                                                                                                                                                                                                                                                                                                                          241 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRR
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Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Glycoprotein; Plasma; Serine protease SIGNAL
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MEDLINE=97009792; PubMed=8856896;
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HSSP; P01009; 1QMB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=SERPINA1; Synonyms=PI;
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P50447;
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                                                                                                                                                                                                                                                                                                                                                                                                                              265 WVLAMDYVATATAFFILPDQGKUHQLEDMLTKEIRAKFLEKRYPSSANLHLPKLTISGTY 324
                                                                                                                                               58 ATAFAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIP 357
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                                                                                                                                                                                                                                                                                                                       178 RDTVFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSS
                                                                                25 EGLQGHAVQETDVPRHDHEQHQEAACHRIAPNLADFAFSLYRQVARQSNTSNIFLSPVTI
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                    Gaps
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Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Protease inhibitor; Serine protease inhibitor; Serpin.
SEQUENCE 413 AA; 45953 MW; B08D2544695EE0F4 CRC64;
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Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
Spermophilus.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358 RSIPPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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72.0%; Pred. No. 5.4e-89;
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                    40; Mismatches
                 286; Conservative
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Best Local S:
Matches 274;
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                        ATAI FFLPDEGKLQHLENELTHDI ITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLG
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STRAIN=Wistar; IISSUE=Liver;
STRAIN=Wistar; IISSUE=Liver;
MEDLINE=91035351; PubMed=2229024;
Misumi Y., Sohda M., Ohkubo K., Takami N., Oda K., Ikehara Y.;
Molecular cloning and sequencing of the cDNA of rat alpha 1-protease inhibitor and its expression in COS-1 cells.";
                                                                                       DKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQCKIVDLVKELDRDTVFALVNY
                                                                                                                                                                         IFFKGKWERPFEVKDTEBEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI _TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1990 (Rel. 15, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Alpha-1-antiproteinase precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor).
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-!- TISSUE SPECIFICITY: Plasma.
-!- SIMILARITY: Belongs to the serpin family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 IFFKGKWKRPFNPEHTRDADFHVDKSTTVKVPMMNRLGMFDMHYCSTLSSWVLMMDYLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 AOKIDISHHDODHPIFNKIIPNLAEFAFSLYRQLAHOSNSTNIFFSPVSIATAFAMLSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 IFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 ATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                             GlCNAc. ..) (Potential) (GlCNAc. ..) (Potential) (GlCNAc. ..) (Potential) (GlCNAc. ..) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1,
                                                                                                                                                                                                                                                                                                                                                                                                                                               411;
                                                                                                                                                                                                                                                                                                                                                                                                                                              71.0%; Score 1443.5; DB 1; Length 69.9%; Pred. No. 6.1e-88; ive 62; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                           Alpha-1-antiproteinase.
Reactive bond.
N-linked (GlCNAC...) (
N-linked (GlCNAC...) (
N-linked (GlCNAC...) (
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25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                   A -> G (in Ref. 2).

M -> I (in Ref. 3).

H -> Y (in Ref. 3).

H -> Y (in Ref. 2).

K -> N (in Ref. 2).

K -> N (in Ref. 2).

K -> N (in Ref. 3).

K -> N (in Ref. 3).
                                                                                     PEGMI, PRODUCES; PROL_INH_Berpin.
PEGMI, PRO0079; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Direct protein sequencing; Glycoprotein; Plasma; Serine protease inhibitor; Serpin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 KPFVFLMIEQNTKSPLFMGKVVNPT 392
                                                                  HSSP; P01009; 10MB.
InterPro; IPR000215; Prot_inh_serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPFIFMIVESETQSPLFVGKVIDPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Serine protease inhibitor alpha 1.
                                                                                                                                                                                       25 411
376 41
64 64
64 64
75 265
4 101
84 18
247
248 K
318 K
318 K
318 K
EMBL; M32247; AAA40788.1;
EMBL; D00675; BAA00579.1;
EMBL; X16273; CAA34349.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.0
Best Local Similarity 69.9
Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                      248
318
322
3411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
                                                   PIR; A33892; ITRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Serpinal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
06AYZS
1D 06AYZS
AC 06AYZZ
DT 25-0C
DT 25-0C
DT 25-0C
DE Serinc
GN Name==
GN Rattu
OC Rukary
OC Mamma
OX NCBI
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Name=Spi2
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P97277;
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P97277
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                      Straubberg R.L., Feingold E.A., Grouse J.G.,

A traubberg R.L., Feingold E.A., Grouse J.G.,

A tracholory S.P., Zeebbrg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A trachol S.F., Zeebbrg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A hopking R.F., Jordan H., Moore T., Max S.I., Wang J., Hsich F.,

A papteron M., Soarse M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

B romatein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,

B Roha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Glibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Noriski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

" "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 EKFLEEVKNNYHSEAFSVNPADSEEAKKVINDYVEKGTQGKIVDLMKQLDEDTVFALNNY 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 IFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 ATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  308 ITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVKFN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82
                                                                                                                                                                                                                                                                                                                                                                TISSUE-Testis;
A Director MGC Project;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
L. SIMILARITY: Belongs to the serpin family.
R GO, GO:000823; F:pepfidase activity; IEA.
R GO, GO:0008867; F:serine-type endopeptidase inhibitor activity; IEA.
R GO; GO:0008867; F:serine-type endopeptidase inhibitor activity; IEA.
R GO; GO:0008867; F:serine-type endopeptidase inhibitor activity; IEA.
R InterPro; IPR000215; Prot_in_serpin.
R Fam; Fr00079; SERPIN; 1.
R SWART; SM00093; SERPIN; 1.
R PROSITE; PS00284; SERPIN; 1.
R Protease; Protease inhibitor; Serine protease inhibitor; Serpin.
CW SEQUENCE 411 AA; 46121 MW; 31637D821BFCB87B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 AQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 1443.5; DB
; Pred. No. 6.1e-88;
62; Mismatches 53
               PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KPFVFLMIEQNTKSPLFMGKVVNPT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.0%;
69.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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RESULT 11 046519

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237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58 ATAFAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 LFLSQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     265 WVLLLDYAGNATAFFILPDQGKLQHLEDTLTKGILARFLGNRHSSFVNVHLPKLSISGTY 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 DLKSVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIP 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TO N.A. Irvin Z.V., Bell T.K., Brandon R.B.;

Giffard J.M., Irvin Z.V., Bell T.K., Brandon R.B.;

Submitted (Aug.1999) to the EMBL/GenBank/DDBJ databases.

C. -! SIMILARITY: Belongs to the serpin family.

REDE, AF034077; AAC83412.1; -.

RHSSP; PO1009; 10MB.

R GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.

InterPor: IPR00079; Serpin; 1.

R SMART; SM00093; SERPIN; 1.

R RASH; SM00093; SERPIN; 1.

R PROSITE; PS00284; SERPIN; 1.

R PROSITE; PS00284; SERPIN; 1.

R PROSITE; SGOOR SERPIN; 1.

R PROSITE; A6942 Serine protease inhibitor; Serpin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 EDLQGCAVQETHATAHDEEHLQEPAEHKIAPNLADFAFSLYRHVAHQSNTTNIFFSPVSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EDPQGDAAQKTDTSHHDQDH----PTFNKITPNLAEFAFSLYRQLAHOSNSTNIFFSPVSI
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                              Būkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 70.9%; Score 1440.5; DB 2; Length Best Local Similarity 69.0%; Pred. No. 1e-87; Matches 274; Conservative 55; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                           Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 AA
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Mesocricetus auratus (Golden hamster).
                                                                                                  Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
PRELIMINARY;
                                                                                             (TrEMBLrel.
                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel.
                                                                                                                                                (TrEMBLrel
                                                                                                                                                                                                                                                                                                                                               Equus caballus (Horse)
                                                                                                                                                                                                                                             Alpha-1-antitrypsin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesocricetus
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Wu Y.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 LKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AKLVDTFLEDVKNLHHSKAFSINFRDAEEAKKKINDYVEKGSHGKIVDLVKDLDQDTVFA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 GQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 LSLGAKGNTHTEILEGLGFNLTELAEAEIHKGFQHLLHTLNQPNHQLQLTTGNGLFINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   206 LVNYISPKGKWEKPPEVEHTTERDFHVNEQTTVKVPMMRLGMFDLHYCDKLASWYLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28 QCHAVQETDDTAHQE--AACHKIAPNLANFAFSIYHKLAHQSNTSNIFFSPVSIASAFAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 LSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 LVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 YLGNATAIFFLPDEGKLOHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVL
                                                                                                                                                                                                                                   Biochem. J. 273:685-690(1991).
-!- FUNCTION: Inhibits human leukocyte elastase, pig pancreatic elastase and bovine trypsin on a 1:1 molar basis.
-!- SUBCELLULAR LOCATION: Extracellular.
-!- TISSUE SPECIFICITY: Plasma.
-!- SIMILARITY: Belongs to the serpin family.
Saunders N.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 1430; DB 1; Length 416; 69.2%; Pred. No. 4.9e-87; ive 62; Mismatches 56; Indels
                                                                                                                                                    MEDLINE-91144555; PubMed-1899999;
Mistry R., Snashall P.D., Totty N., Guz A., Tetley T.D.;
"Isolation and characterization of sheep alpha 1-proteinase
            Brown W.M., Dziegielewska K.D., Foreman R.C., Saunders N.R. "Nucleotide and deduced amino acid sequence of sheep alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -> S (in Ref. 2).
-> A (in Ref. 2).
0B4702C0527321BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GlcNAc. . .) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alpha-1-antiproteinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
N-linked (GlcNAc...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct protein sequencing, Glycoprotein, Plasma, Serine protease inhibitor, Serpin, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reactive bond
                                                                        Nucleic Acids Res. 17:6398-6398(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P01009, IQMB.
InterPro; IPR000215; Prot_inh_serpin.
Pfam, PF000079; Serpin; 1.
PRNOSTE; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
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381
68
105
143
N 143
N 269
N 269
A 269
A 5984 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15555; CAA33561.1; -. PIR; S05312; ITSH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 69.2
hes 269; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45
416 AA;
                                                                                                                SEQUENCE OF 25-55.
                                                                                                                                       TISSUE=Plasma;
                                                       antitrypsin."
                                                                                                                                                                                                                    inhibitor.";
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLV 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDTVFALVNY 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 ATAIFFLPDEGKLOHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSIPPEVKFN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 DKFLEEVKNDYHSEAFSVNFTDSEEAKKVINGFVEKGTGGKIVDLVKDLDKDTVLALVNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     207 IFFKGKWKKPFDADNTEEADFHVDKTTTVKVPMMSRLGMFDVHYVSTLSSWVLLMDYLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    267 ATAIFILPDDGKMQHLEQTLNKEIIGKFLKDRHTRSANVHFPKLSISGTYNLKTALDPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPPKGKWERPFBVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                 MEDLINE=96004896; PubMed=7548212; DOI=10.1016/0167-4781(95)00140-C; Nakatani T., Suzuki Y., Yoshida K., Sinohara H.; "Molecular cloning and sequence analysis of cDNN encoding plasma alpha-1-antiproteinase from Syrian hamster: implications for the evolution of Rodentia."; Biochim. Biophys. Acta 1263:245-248(1995).
-1-SIMILARITY: Belongs to the serpin family.
PIR; S60036; S60036.
                                                                                                                                                                                                                                                        HSSP; P01009; 1QMB.
GO: GO:000867; F:serine-type endopeptidase inhibitor activity; IEA.
InterPro; IPR00015; Prot_inh_serpin.
Pfam; PF00079; Serpin; 1.
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01-0CT-1989 (Rel. 12, Last sequence update)
01-0CT-1989 (Rel. 14, Last sequence update)
05-JUL-2004 (Rel. 14, Last annotation update)
Alpha-1-antiproceinase precursor (Alpha-1-antitrypsin) (Alpha-1-proteinase inhibitor)
0701s arise (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 413;
                                                                                                                                                                                                                                                                                                                                      SMART; SM00093; SERPIN; 1.
Protease inhibitor; Serine protease inhibitor; Serpin; Signal.
SIGNAL 1 24 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  alpha-1-antiproteinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             70.4%; Score 1431.5; DB; 70.2%; Pred. No. 3.9e-87; tive 55; Mismatches 59.
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MEDLINE=89366677; PubMed=2788872;
                                                                                                                                                                                                                                                                                                                                                                                                                       413 AA; 45819 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 271; Conservative
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                             SEQUENCE FROM N.A.
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P12725;
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SEQUENCE
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OX NCBI
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RP SEGI

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188 IFFKGKWERPFEVKDTEBEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVLLMKYLGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=64680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=CM55-MM;
                                                                                 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 DKFLEDVKSLYHSEALPTNFTNFTNTEBARQQINSYVEKGTQGKIVELVKELHRDTVLALVNY 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 TKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFLSQGLKLV 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alpha-1-antitrypsin-like protein CMS5-WM.
Reactive bond (By similarity).
Pyrrolidone carboxylic acid (Potential).
N-linked (GlcNac. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      carboxylic acid; Serine protease inhibitor;
                                                                                                                                                                                                      30-MAY-2000 (Rel. 39, Created)
25-OMY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last amotation update)
Alpha-1-antitrypsin-like protein CMS5-MM precursor.
Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.2%; Score 1427; DB 1; Length 413; 69.6%; Pred. No. 7.7e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46212 MW; D1C37B899BB20B69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 204:127-132[1997].
-!- TISSUE SPECIFICITY: Expressed in liver.
-!- SIMILARITY: Belongs to the serpin family.
                                                                                                                                                                  413 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Mismatches
                                            |:||:||:|||
386 VEFNRPFLCILYDRNTKSPLFVGKVVNPT 414
                         VKFNKPFVFLMIEQNTKSPLFMGKVVNPT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potential,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P01009; 1QMB.
InterPro; IPR00215; Prot_inh_serpin.
Pfam; PP00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
SMART; SR00284; SERPIN; 1.
Glycoprotein; Pyrrolidone carboxylic serpin; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB000546; BAA24416.1; -.
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                                                                                                                                                                  STANDARD;
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413
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266
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                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=64680;
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                                                                       ATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLKSVLGQLG
207 IFFKGKWEEPPINEEDTKEEDFHVDEATTVRVPMMNRLGMFHLHHCSTLASWVLQMDYLGN
                                                                                                     8 AQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATAFAMLSLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0004867; F:serine-type endopeptidase inhibitor activity; IEA.
InterPro; IPR000215; Prot_inh_serpin.
Pfam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tamias sibiricus (Siberian chipmunk) (Asian chipmunk).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Sciurinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
PubMed=15033530; DOI=10.1016/j.gene.2003.12.010;
Nakazawa A., Inaba Y., Kamijima A., Kondo N., Ito M., Shiba T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ő
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00284; SERPIN; 1.
Protease inhibitor; Serine protease inhibitor; Serpin.
SEQUENCE 413 AA; 46208 MW; 61F6FB2DC9F51C25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Alphal-antitrypsin-like protein.
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EMBL; AB100364; BAD06477.1; -.
HSSP; P01009; 1KCT.
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Gene 329:71-79(2004).
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Search completed: June 20, 2005, 19:45:54 Job time : 175 secs

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Ade08102 Novel pro Aaw23649 Recombina

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The present sequence is alpha-1 antitrypsin mutated variant Portland (also termed PDX). This effectively inhibits furin endoprotease. Peptides or peptide mimetics derived from this sequence inhibit bacterial toxins that are processed at a consenus furin recognition site, when administered in therapeutically effective amounts. Portland protein designing the PISPL program and the crystal structure analysed for designing the pharmacophore for the reactive site loop of the Portland variant. Endoproteolytic activation of bacterial toxins and endolytic mimetics. This is useful in treating infections of cells by bacteria (specifically Corynebacterium diptheriae, Bacillus anthracis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alpha-1 antitrypsin variant Portland; alpha-1 antitrypsin; PDX; protease inhibitor; furin endoprotease; peptide mimetic; bacterial toxin; furin recognition site; portland protein; SYBYL program; pharmacophore; protein crystal structure analysis; reactive site loop; RSL; endolytic maturation; endoprotelytic activation; Pseudomonas aeruginosa; Corynebacterium diptheriae; Bacillus anthracis; cytomegalovirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New furin endoprotease inhibitor that mimics a specific region of alphalantirypsin Portland mutant, for treatment and prevention of bacterial and viral infection.
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                FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL
                                                                                                                    SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT
                                                                                                                                                                                                                                                                              SVLGQLGITKVFSNGADLSGVTBEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI
                                                    FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL
                                                                                                       SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT
                                                                                                                                                                                 181 VFALVNYIPFKGKWERPFEVKDTEBEDPHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL
                                                                                                                                                                                                            LMKYLGNATAI FFLPDEGKLQHLENELTHDI ITKFLENEDRRSASLHLPKLSITGTYDLK
 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
                                                                                                                                                           VPALVNYI PPKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL
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Query Match 100.0%; Score 2032; DB 2; Length 394; Best Local Similarity 100.0%; Pred. No. 5.5e-158; Matches 394; Conservative 0; Mismatches 0; Indels 0.

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inhibition assay to assess the biological activity of the peptide mimetics. A7 cells when incubated with PIT exhibited little or no protective effect in the presence of Pseudomonas aeruginosa exotoxin A. PIT was also used as a negative control for the assay to detect PDX - mediated inhibition of furin-catalysed maturation of HCMV glycoprotein gB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature protein sequence of alphal-antitrypsin (AAT)
                                                                                                                           Score 2026; DB 2;
Pred. No. 1.7e-157;
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97US-0038168P.
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Best Local Similarity 99.7%;
Matches 393; Conservative
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The present sequence represents the mature protein of alphal-antitrypsin (AAT). The protein is used to exemplify the invention. The specification of describes a method for producing mature heterologous protein in monocotyledomous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledom transcription regulator, inducible either during seed maturation or by adding/removing a small colecule, DNA encoding the heterologous protein, and DNA encoding a signal peptide, with the signal peptide causing secretion of the protein completed, with the signal peptide causing secretion of the protein completed, with the signal peptide causing secretion of the protein completed alpha 1-antitrypsin (ART) with a glycosylation pattern that significantly increases its serum half-life, mature glycosylated antithrombin III (ATII), mature human serum albumin (HSA) having the native folding pattern as shown by bilirubin-binding characteristics, or mature active subtilisin BPN. These proteins are useful therapeutically control of the promoter active subtilisin BPN. These proteins are useful therapeutically control of the promoter active subtilisin BPN. These proteins are useful therapeutically control of the protein control of the protein control of the c
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                                                                           Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     replacement) or as industrial enzymes (BPN' is used in detergents)
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Best Local Similarity 98.5%; Pred. No. 1.3e-155;
Matches 388; Conservative 3; Mismatches 3;
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                                                                                                                                                                                         Disclosure; Page 28-29; 53pp; English
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WPI; 1998-467179/40.
N-PSDB; AAV41726.
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2002-500631/53 N-PSDB; ABK88015

otitis media, otitis external, HIV; psoriasis; human immunodeficiency virus; atopic dermatitis; muscular dystrophy; herpes; ulceration; sepsis; rheumatoid arthritis; periodontal disease; tumour metastas; tumour angiogenesis; osteoporosis; Paget's disease; glomerulonephritis; scleroderma; Alzheimer's disease; hypertension. Pemberton P; 18-DEC-2000; 2000US-0256699P. 20-NOV-2001; 2001US-0331966P. 18-DEC-2001; 2001WO-US049256. (ARRI-) ARRIVA PHARM INC. Barr PJ, Gibson HL, WO200250287-A2 Homo sapiens. 27-JUN-2002.

Novel fusion protein useful for inhibiting protease activity associated with a disorder such as emphysema, asthma, comprises a first protease inhibitor comprising alpha 1-antitrypsin and a second protease inhibitor.

Claim 25; Page 25-27; 134pp; English.

protease inhibitor comprising an alternative control to protease inhibitor or its functionally active portion and a second protease inhibitor or its functionally active proteins and a second protease inhibitor or its functionally active protease activity. The fusion protein of the invention may act as an inhibitor of protease activity. The fusion protein of the invention is useful for inhibiting protease activity associated with a disorder such as complysemma, askimma, chronic obstructive pulmonary diseases, cystic fibrosis, oitis madia, otitis external or HIV infection, or for treating an individual suffering from or at risk for a disease or disorder convolung unwanted protease activity. The proteins are useful for treating dermatological diseases such as atopic dermatitis, eczema and parating dermatological diseases such as atopic dermatitis, eczema and convolung in inflammatory responses to viral infection, and for treating wounds, sepsis, rheumatoid arthritis, periodontal disease, tumour metastasis and tumour anglogenesis, gastric ulceration, osteoporosis, paget's disease, glomerulonephritis, gastric ulceration, advanced infection, alzheimer's disease, hypertension and muscular dystrophy. The present sequence represents the human alpha-1-antitrypsin (AAT) protein cuest to create the fusion protein of the invention This invention relates to a novel fusion protein comprising a first

Sequence 394 AA;

FAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFPSPVSIATA FAMLSLGTKADTHDE1LEGLNFNLTO1PEAQ1HEGFOELLRTLNOPDSQLQLTTGNGLFL SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT VFALVNY I FFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL VFALVNYI FFKGKWER PFEVKDTEBEDFHVDQVTTVKVPMMKRLGMFNI QHCKKLSSWVL EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA Gaps .. Length 394; 3; Indels Score 2003; DB 5; Pred. No. 1.3e-155; 98.5%; Scor. No. 1... 98.5%; Pred. No. 1... 3; Mismatches Matches 388; Conservative Local Similarity Н 61 61 181 Query Match 121 g g 8 δ à g Š

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LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300

241

SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI Mouse alpha-1-antitrypsin (AAT) mature protein SEQ ID NO:4. PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 394 ADM82878 standard; protein; 398 29-JUL-2004 301 ADM82878; 361 301 ADM82878 RESULT 셤 g ò ò

alpha 1-antichymotrypsin; ACT; alpha 1-antitrypsin; AAT; gene therapy; protein therapy; diabetic ulcer; arterial ulcer; ulcus cruris arteriosum; necrobiosis lipoidica; ulcera arteriousa; wound healing; human.

Homo sapiens.

EP1415664-A1.

06-MAY-2004.

30-OCT-2002; 2002EP-00024200.

30-OCT-2002; 2002EP-00024200.

(SWIT-) SWITCH BIOTECH AG.

Halle J, Goppelt A;

WPI; 2004-341870/32. N-PSDB; ADM82879. Use of alpha 1-antichymotrypsin polypeptide in combination with alpha 1-antitrypsin polypeptide for treating and/or preventing poorly healing diabetes-associated and/or poorly healing arterial wounds e.g., diabetic

Claim 2; SEQ ID NO 4; 31pp; English.

The present invention describes a method of using alpha 1antichymotrypsin (ACT), its functional variant and/or encoding nucleic
antichymotrypsin (ACT), its functional variant and/or encoding nucleic
acid, in combination with alpha 1-antitrypspin (AAT), its functional
caid, in combination with alpha 1-antitrypspin (AAT), its functional
caid, in combination with alpha 1-antitrypspin (AAT), its functional
correction or its encoding nucleic acid, for treating and/or preventing
copypeptide or its encoding nucleic acid, for treating and/or preventing the diseases, where the ACT polypeptide or its encoding
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cucle acid or a cell expressing the AAT polypeptide or its encoding
cucleic acid is combination) are useful for treating and/or
cacid or a cell expressing the AAT polypeptide or its encoding
cucleic acid as diabetes associated and/or poorly healing
cuterial wounds such as diabetic ulcer and arterial ulcer, preferably
clabetic ulcer. Diabetic ulcers are skin lesions in mammals and humans
cuffering from diabetes (e.g., include ulcus cruris arteriosum,
caused by arteriosclerotic destruction of the blood vessels. The present
cevemplification of the present invention.

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Location/Qualifiers
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                                                                                            Disclosure; Fig 1A; 48pp; English
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(first entry)
   N-PSDB; AAN40078.
                                                                                                                                                                                                                         Sequence 418 AA;
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28-JUN-1990
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Matches
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                                                                                                                             BPPQGDAAQKIDISHHDQDHPTFNKITPNLABFAFSLYRQLAHQSNSTNIFFSPVSIATA
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                                                                           Gaps
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                                      Length 398
                                                                           3; Indels
                                    Score 2003; DB 8;
Pred. No. 1.3e-155;
3; Mismatches 3;
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(BGHM ) BRIGHAM & WOMENS HOSPITAL.
(KAWA/) KAWASAKI G H.
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    /label= signal
    .418

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88EP-00201179.
82US-00409183.
83US-00489406.
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98.5%;
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(first entry)
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                                Query Match
Best Local Similarity 98.5
Matches 388; Conservative
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Sequence 398 AA;
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13-AUG-1982;
18-AUG-1982;
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16-PEB-1992
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                                                                                                                                                         The inventors claim a DNA construct contg. a gene encoding human alpha-1-antitrypsin. A substantially pure, substantially unglycosylated mammalian alpha-1-antitrypsin is also claimed. (Updated on 25-MAR-2003 to correct
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Extra:chromosomal element for replication in yeast - with yeast promoter for regulation of glycolytic protein prodn.
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Predominant form of human alpha-1-antitrypsin as encoded by cDNA.

Human alpha-1-trypsin (hAT); anti-AT antibodies; proteolytic activity; AT deficiency; Saccharomyces cerevisiae GK 100; 2-mu plasmid DNA; CATI; plasmid HAT4; yeast TPI promoter; yeast TPI terminator; plasmid C1/1.

pdx1.rag

(first entry)

21-DEC-1999

AAY26925;

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produce of a mammalian alpha-lance of AT). Also claimed is the produce of a mammalian alpha-lance of AT). Also claimed is the produ. of polypeptides having the protease-inhibiting activity of a mammalian AT. A culture of microorganisms is grown such as fungi or yeast, esp. Saccharomyces cerevisiae GK 100, which are transformed with a DNA transfer vector 2-mu plasmid, plasmid CATI or plasmid HAT4, contg. a segment encoding the mammallan AT. The unglycosylated polypeptides are useful for produ. of anti-AT antibodies, for modulating proteolytic activity in mammals, and for treating AT deficiency, esp. for replacing TAT4, the diven example plasmid HAT4 comprises the yeast promoter, an ATGGAGGATC adapter, the hAT gene and the yeast promoter, an ATGGAGGATC adapter, the hAT gene and the yeast promoter, an argine of 101, which contains the entire 2-mu DNA from S. cerevisiae. S. cerevisiae GK100 transformed with HAT4 produces soluble protein with an hAT content of 2-3* when grown on a medium contg. 6* glucose. (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
                                                                                                                                                                                                                                                                                                                         in the patent are unglycosylated polypeptides having the amino acid
                                                                                                                                                                                                                    New alpha-1-antitrypsin polypeptide(s) - produced by recombinant DNA techniques, esp. using yeast host.
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Pred. No. 1.4e-155;
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                  82US-00408099.
83US-00489406.
                                                                                                                      Woodbury RG;
                                                                               (ZYMO ) ZYMOGENETICS INC.
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                                                                                                                      Kawasaki GH,
                  13-AUG-1982;
28-APR-1983;
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                                         FAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL
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                           EDPOGDAAOKTOTSHHDODHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
Gaps
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AAY26925 standard; protein; 418 AA

RESULT 8
AAY26925
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This sequence represents the coding region of the human alpha-1-antitrypsin (AT) gene. The invention relates to the production of AT in plant cheells, especially monocovyledonous plants. Also produced are variants of the AT protein, in which the glycosylation pattern of the protein is altered. AT inhibits serine proteases, specifically neutrophil elastase (but also trypsin, cathepsin G, thrombin etc.) so protect pulmonary tissue against protease damage. Are used to treat AT-deficiency conditions, particularly pulmonary emphysema, cystic fibrosis, septic shock and rheumatism. The use of plants for the recombinant production of AT results in a product without risk of (sub)viral contamination. The recombinant AT had good activity and is stable, with low immunogenicity (associated with glycosylation patterns similar to the native protein)
                                                                                             Human; alpha-1-anti-trypsin; transgenic plant; monocotyledon; variant; glycosylation; serine protease; inhibitor; neutrophil; elastase; trypsin; cathepsin G; thrombin; pulmonary tissue; protease damage; septic shock; pulmonary emphysema; cystic fibrosis; rheumatism; recombinant;
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                                                                                                                                                                                                                                                                                                                                    note= "putative glycosylation site"
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98.5%; Pred. No. 1.4e-155;
ive 3; Mismatches 3;
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                                                                Human alphal-anti-trypsin type M1 protein.
                                                                                                                                                                 virus contamination; immunogenicity; ss
                                                                                                                                                                                                                                                                                   5. .418
|abel= mature protein
                                                                                                                                                                                                                                                  1. .24
/label= signal_peptide
                                                                                                                                                                                                                               location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MERI-) MERISTEM THERAPEUTICS
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Matches 388; Conservative
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Active-site
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204 240 384

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Human; ovarian cancer; marker; cancer; familial history; brain disorder; central nervous system disorder; bacterial meningitis; viral meningitis; Alzheimer's disease; Parkinson's disease; cerebral oedema; hydrocephalus; brain herniation; inflammation; encephalitis; testicular disorder; nontuberculous granulomatous orchitis; connective tissue disorder; heart disorder; ischaemic heart disease; atherosclerosis; neoplasm; histological type; carcinogenic; ovarian cancer marker.
                                                                                                                                                        205 VFALVNYIFFKGKWERPPEVKDTEEEDFHVDQVTTVKVPWMKRLGMFNIQHCKKLSSWYL 264
                                                                                                                                                                                                                                              LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
                                                                                                                                                                                                                                                                                 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 324
                                                                                                                                                                                                                                                                                                                                                                   SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI 360
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                               SEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTGGKI VDLVKELDRDT
                                                                                                                        VPALVNY I PPKGKWERPPEVKOTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL
                                                                                                                                                                                                                                                                                                                                                                                                   325 SVLGQLGITKVFSNGADLSGVTEBAPLKLSKAVHKAVLTIDEKGTBARGAMFLEAIPMSI
   SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT
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Morrisey MP, Olandt PJ, S
Lu K, Schmandt RE, Zhao X,
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26-SEP-2001; 2001US-0324967P.
26-SEP-2001; 2001US-0325102P.
26-SEP-2001; 2001US-0325149P.
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2001US-0311732P.
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10-AUG-2001;
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The present invention relates to a new method for assessing whether

Disclosure; Page 403-404; 481pp; English

non cancer patient

from a

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the expression level of a marker in a patient sample and the normal level

C f expression of the marker in a control non-ovarian cancer sample, where

C the marker is selected from 363 cancer markers described in the

c therecterising cancer, in detecting the presence of cancer as early as

C characterising cancer, in detecting the presence of cancer as early as

C possible, and the recurrence of ovarian cancer rate said be of

particular use with patients having an enhanced risk of developing

C ovarian cancer (e.g. patients having an enhanced risk of developing

C cancer). The cancer markers may be used in the management and treatment

C e.g. brain and central nervous system disorders (e.g. bacterial and

C e.g. brain and central nervous system disorders (e.g. bacterial and

C inflammations (e.g. bacterial or viral meningitis or encephalitis),

Inflammations (e.g. bacterial or viral meningitis or encephalitis),

C connective tissue disorders, or heart disorders (e.g. ischaemic heart

C sused in assessing the histological type of neoplasm associated with

C varian cancer has meteataalized or is likely to metastasize,

C used in assessing the histological type of neoplasm associated with

C varian cancer has meteataalized or is likely to metastasize,

C whether ovarian cancer has metastasized or is likely to metastasize,

C varian carcinogenic potential of a compound, or inhibiting ovarian

C cancer raptresents one of the ovarian cancer markers described in the
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ilarity 98.5%; Pred. No. 1.4e-155;
Conservative 3; Mismatches 3;
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es 388; Conserv
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peptide. The method involves removing a saccharyl subunit from the peptide, thus forming a truncated glycan, and contacting the truncated glycan, and contacting the truncated control of glycan with at least one glycosyltaneferase and at least one glycosyl donor conditions suitable to transfer at least one glycosyl donor to the truncated glycan, thus remodeling the peptide. Conjugates can be formed between a granulocyte colony stimulating factor (G-CSP) peptide, interferon beta peptide, reactor (G-CSP) peptide, conterferon beta peptide, expenied, granulocyte macrophage colony stimulating factor (MrcSP) peptide, granulocyte macrophage colony stimulating factor (MrcSP) peptide, interferon-gamma peptide, tissue plasminogen activator (TPA) peptide, interferon-gamma peptide, tissue plasminogen activator (TPA) peptide, interferon-gamma peptide, tissue plasminogen activator (TPA) peptide, interfleukin-2 (IL-2) peptide, vill peptide, interfleukin-2 (IL-2) peptide, urckinase peptide, anti-caceptor/immunoglobulin (IG) G fusion peptide, chimeric anti HERZ creceptor/immunoglobulin (IG) G fusion peptide, anti-colonal antibody peptide, anti-colonal antibody peptide, recombinant DNase peptide, anti-TNF alpha peptide, insulin peptide, recombinant DNase peptide, anti-TNF alpha peptide, insulin peptide, and a modifying group, where the modifying group is covalently attached to the peptide through an intact glycosyl linking group. The method is useful for a cell-free, in vitro method of the colon colo ö Remodeling a peptide, by removing a saccharyl subunit from the peptide to form truncated glycan, and adding or deleting glycosyl groups to a peptide and/or adding modifying group of a peptide to remodel the 61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120 85 PAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELRTLNQPDSQLQLTTGNGLFL 144 9 25 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA 84 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA invention relates to a cell-free, in vitro method of remodeling a Gaps ö Length 418; Chen X; 3; Indels Bowe C, Hakes D, Score 2003; DB 6; Pred. No. 1.4e-155; Query Match

98.6%; Score 2003; L
Best Local Similarity 98.5%; Pred. No. 1.4e
Matches 388; Conservative 3; Mismatches human A-1-PI or alpha-antitrypsin Example; Fig 61B; 900pp; English. Bayer R, (NEOS-) NEOSE TECHNOLOGIES INC 2001US-0344692P. 2001US-033423P. 2001US-0334201P. 2002US-0334301P. 2002US-0391777P. 2002US-0404249P. 28-AUG-2002; 2002US-0407527P. 2002WO-US032263 2001US-0328523P De Frees S, Zopf D, WPI; 2003-449162/42. N-PSDB; ACC78879. Sequence 418 AA; WO2003031464-A2. 07-JUN-2002; 25-JUN-2002; 17-JUL-2002; Homo sapiens. 09-OCT-2002; 19-OCT-2001; 28-NOV-2001; 10-OCT-2001; 28-NOV-2001; 17-APR-2003 16-AUGð g ò 요 ઠે

SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180 121

300 360 324 384 145 SEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDT 204 100 VPALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI VPALVNY I FFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNI QHCKKLSSWVL LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394 325 385 265 181 241 301 361 셤 셤 ò g ò g ò ò

ADB99858 standard; protein; 418 AA ADB99858 ID ADB

ADB99858;

(first entry) 04-DEC-2003 Human alpha-1-antitrypsin protein.

neurodegenerative disease; protease inhibitor; nootropic; neuroprotective; antiparkinsonian; anticonvulsant; Alzheimer's disease; Pick's disease; Huntington's disease; Parkinson's disease; alpha-1-antitrypsin; aaT; gene therapy.

Homo sapiens.

WO2003028621-A2.

30-SEP-2002; 2002WO-EP010937.

01-OCT-2001; 2001DE-01048553

(PROT-) PROTAGEN AG

Zabel C; Klose J, Meyer H,

WPI; 2003-371960/35. N-PSDB; ADB99860.

Composition for treating or preventing neurodegeneration, e.g. Alzheimer's or Parkinson's diseases, contains protease inhibitor, especially alphal-antitrypsin.

Claim 6; SEQ ID NO 2; 40pp; German.

This invention describes a novel composition for treatment or prevention of neurodegenerative disease containing at least one protease inhibitor and which has nootropic, neuroprotective, antiparkinsonian and anticonvulsant activity. The compostions are specifically used to treat or prevent Alzheimer's, Pick's, Huntington's and Parkinson's diseases and also for diagnosis. DNA sequences that encode alpha-1-antitrypsin (aaT), or its fragments, are useful for isolating homologous RNA or DNA sequences, and for recombinant production of aaT in gene therapy. This sequence represents the human alpha-1-antitrypsin (SWISS PROT No: P01009) used in the composition of the invention.

Sequence 418 AA;

ö Gaps ö Length 418; Indels Query Match

98.6%; Score 2003; DB 7;
Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3;

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FAMI.SLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120

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EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQIAHQSNSTNIFFSFVSIATA

EDPOGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA

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85 FAMLSLGTKADTHDBILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL

SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180

VPALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 264 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSIIGTYDLK 300 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 324 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI 360 325 SVLGQLGITKVPSNGADLSGVTEBAPLKLSKAVHKAVLTIDEKGTBAAGAMFLEAIPMSI 384

205

181

265

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301

385 PPEVKENKPFVFLMIEQNTKSPLFMGKVVNPTQK 418 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394

361

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ADE63536 standard; protein; 418

RESULT 12

ADE63536;

144

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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell
                                                                                                                                                                                                                                                                                                                                                                                                                                           New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                          Costigan M;
                                                                                          Human Protein P01009, SEQ ID NO 9480.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                 (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                          Woolf C, D'urso D,
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GENBANK; P01009.
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                                                                                                                                                                         Homo sapiens.
                                                                29-JAN-2004
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for

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comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to be perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal completed to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating cartivity in an animal of one or more of the polypeptides or their antibodies. The polynucleotide or the compound that security is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that configures in e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene configuration, but was equence presented is a human protein (shown in Table 2 of the specification) but was obtained in electronic form directly from WIPO at
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Best Local Similarity 98.5%; Pred. No. 1.4e-155;
Matches 388; Conservative 3; Mismatches 3;
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or human polynuclectides or composition computating two or more instruction of the nucleic acid sequence. Also derivative or allelic variation of the nucleic acid sequence. Also calaimed are a vector comprising the novel polynuclectide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynuclectide sequence that is differentially expressed in neuronal tissue of a first animal compound of a polynuclectide sequence which is differentially expressed in animal subjected to pain, a method for identifying a compound which regulates the expression of a polynuclectide sequence which is differentially expressed in animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynuclectides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of the polypeptides given in the activity in an animal of one or more of the polypeptides given in the apprehence of the paramaceutical composition comprising the one or more polypeptides or their antibodies. The polymuclectide or the compound that modulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_general control control control of the printed specification, but was obtained in electronic form directly form WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
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26-NOV-2001; 2001US-0333347P.
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                                                WO2003016475-A2
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  Homo sapiens.
                                                                                                 27-FEB-2003.
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EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA Gaps ; 0 Length 418; Score 2003; DB 7; Length 41 Pred. No. 1.4e-155; 3; Mismatches 3; Indels Query Match 98.6%; Best Local Similarity 98.5%; Matches 388; Conservative ઠે

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SOGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTOGKIVDLVKELDRDT

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241 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300 265 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 324 325 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI 384 205 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 264 SVLGQLGITKVFSNGADLSGVTEBAPLKLSKAVHKAVLTIDEKGTBAAGAMFLERIPRSI PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394 385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418 361 301 ò 유 δ 임 ò g

ADE63532 standard; protein; 418 AA ADE63532; ADE63532

Costigan M;

Befort K,

(first entry) 29-JAN-2004 Human Protein P01009, SEQ ID NO 9476.

Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Homo sapiens.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765

14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P.

(GEHO) GEN HOSPITAL CORP. (FARB) BAYER AG.

Befort K, Costigan M; Woolf C, D'urso D,

WPI; 2003-268312/26. GENBANK, P01009. New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polyneptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more pain and a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound that

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modulates its activity is useful for preparing a medicament for treating plun (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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Pred. No. 1.4e-155;
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                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Protein P01009, SEQ ID NO 9468.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADE63524 standard; protein; 418 AA
                                                                                                                                                                   98.6%;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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                                                                                                                                                                                              Matches 388; Conservative
                                                                                                                                                                                   Local Similarity
                                                                                                                                        Sequence 418 AA;
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, or human polynucleotides or a polynucleotide acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence the expression of a polynucleotide sequence which is differentially expression of a polynucleotide or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more plain and a pharmaceutical composition comprising the one or more polymeptides or their antibodies. The polynucleotide or the compound that confirm (c.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed the sequence data for this patent did not form part of the printed to the sequence data for this patent did not form part of the printed to the content of the printed to the content of the printed to the content o
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                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  85 FAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL
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Costigan M;
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                                                                                                                                                                                            Claim 1; Page; 1017pp; English.
Befort K,
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Best Local Similarity 98.5
Matches 388; Conservative
D'urso D,
                                                WPI; 2003-268312/26
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

June 20, 2005, 19:40:45; Search time 43 Seconds (without alignments) 683.994 Million cell updates/sec

Perfect score:

1 EDPQGDAAQKTDTSHHDQDH.....IEQNTKSPLFMGKVVNPTGK 394

Sequence:

Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

513545 seqs, 74649064 residues

Searched:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Database

Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 9, Appli Sequence 11, Appl Sequence 9, Appli Sequence 6, Appli Sequence 19, Appl Sequence 13, Appl Sequence 13, Appl Sequence 17, Appl , Appli Sequence 11, Sequence 6, A Sequence 1, A Sequence 3, A Sequence 3, A Description Sequence Sequence Sequence Sequence Sequence S Sequence 1 Sequence 1 Sequence 1 Sequence 5 Sequence 5 Sequence Sequence Bequence Sequence Sequence Sequence Sequence 1 US-08-481-534-9
US-08-481-534-11
US-08-481-534-6
US-08-002-202-9
US-08-002-202-6
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US-09-949-016-8165 SUMMARIES Length Query Match Result No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /label=Variant.
OTHER INFORMATION: / note="The amino acid sequence is the amino acid OTHER INFORMATION: sequence of the modified alpha-1-antitrypsin OTHER INFORMATION: protein, alpha-1-antitrypsin Portland."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
                                                            US-08-481-534-9

Sequence 9, Application US/08481534

Patent No. 6022855

GENERAL INFORMATION:

APPLICANT: Thomas, Gary

APPLICANT: Anderson, Eric D

APPLICANT: Hayfilck, Joel S

APPLICANT: Stendlen, Stephan G

TITLE OF INVENTION: Endoprotease

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSER: ADDRESS:

STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2032; DB 3; Length 394; 100.0%; Pred. No. 6.4e-184; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTE: TEACHBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEB PC compatible
COMPUTER: IEB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,534
FILING DATE: 14-SEP-1995
CLASSIFICATION: 530
ATTONEY/AGENT INFORMATION:
NAME: NO. 6022855nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 110PROMATION:
TELEFEXX: 312-913-0001
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LOCATION: 355..358
OTHER INFORMATION: /labe
OTHER INFORMATION: /not
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LENGTH: 394 amino acids
TYPE: amino acid
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Matches 394; Conservative
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181 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
181 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
                                                                                                                                301 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI 360
                                                                                               241 LMKYLGNATAIFFLFDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
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                                                                                                                                                                                                 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI
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APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Havilick, Joel S
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: MODORNEL! Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.7%; Score 2026; DB 3; Length 394; 99.7%; Pred. No. 2.4e-183;
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/481,534

FILING DATE: 14-SEP-1995

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: No. 6022855nan, Kevin E

REGISTRATION NUMBER: 35,303

REFERENCE/DOCKET NUMBER: 92,448-D

TELECOMMUNICATION INFORMATION:

TELEPAR: 312-913-0002
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Chicago
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 11, Application US/08481534
; Patent No. 6022855
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LOCATION: 355..358
OTHER INFORMATION: /labe
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Best Local Similarity
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STATE: IL
COUNTRY: US
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COUNTRY: USA
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                                           EDPQGDAAQKTDTSHHDQDHPTFNKI TPNIAEFAFSLYRQLAHQSNSTNI FFSPVSI ATA
                                                                                              61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL
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                            EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIFICATION: 514
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STREET: 10 South Wacker Drive, Suite 3000
Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
TELEPRA: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
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NAME: NO. 5604201nan, Kevin E
REGISTRATION NUMBER: 35,30003
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393; Conservative
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TOPOLOGY: linear
MOLECULE TYPE: protein
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STATE: Illinois
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                                                                                        /label= Variant
//note= "This amino acid sequence is the amino acid sequence of the modified alpha-1-antitrypsin protein, alpha-1-antitrypsin Portland;"
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                                                                                                                                                                                                                                                      99.5%; Score 2021; DB 1; Length 394; 99.5%; Pred. No. 7.1e-183; ive 1; Mismatches 1; Indels
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GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Stenglen, Stephan G
ITILE OF INVENTION: Methods and Reagents for Inhibit:
TITLE OF INVENTION: Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAETENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,534
FILING DATE: 14-SEP-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
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US-08-481-534-6
; Sequence 6, Application US/08481534
; Patent No. 6022855
                                                                                                                                                                                                                                                                                       Best Local Similarity 99.5
Matches 392; Conservative
REATURE:
NAME / KEY:
DOCATION:
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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Matches 391; Conservative
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US-08-002-202-6
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ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    Score 2020; DB 3;
Pred. No. 8.8e-183;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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10 South Wacker Drive, Suite 3000
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APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laural
APPLICANT: Hayflick, Joel S
TITLE OF INVENTION: Methods and Reagents
TITLE OF INVENTION: Purin Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                            REFERENCE/DOCKET NUMBER: 92,448-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-002-202-11; Sequence 11, Application US/08002202
Sequence 11, Application US/08002202
Patent No. 5604201; GENERAL INFORMATION:
6022855nan, Kevin E
                                                                                                                INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 394 amino acids

TYPE: amino acid

TYPE: amino acid

MOLECULGY: linear

WOLECULE TYPE: protein
                                                                                                                                                                                                                                                         99.4%;
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 99.5'
Matches 392; Conservative
               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Chicago
STATE: Illinois
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61 PAMLSLGTKADTHDEILEGLNFNLTEIPERQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Variants
/note= "This amino acid sequence is the amino
sequence of the modified alpha-1-antitrypsin
variant, alpha-1-antitrypsin Pittsburgh"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.2%; Score 2015; DB 1; Length 394; 99.2%; Pred. No. 2.6e-182; ive 1; Mismatches 2; Indels
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APPLICANT: Thomas, Garry
APPLICANT: Anderson, Eric D
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
TITLE OF INVENTION: Methods and Reagents for Inhibiting
TITLE OF INVENTION: Purin Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
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                                      CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: No. 5604201nan, Kevin E
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,448
TELECOMMUNICATION INFORMATION:
TELEBHONE: 312-715-1000
TELEBHONE: 312-715-1000
TELEBHONE: 312-715-1000
TELEBHONE: 312-715-1000
TELEBHONE: 312-715-1000
TELEBHONE: 312-715-1014
TELECX: 910-221-5317
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
NOLECULE TYPE: protein
FEATURE:
NAMES/KRY: Protein
FEATURE:
NAMES/KRY: Protein
COTHER INFORMATION: /note= "This
OTHER INFORMATION: variant, alf
OTHER INFORMATION: variant, alf
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APPLICATION NUMBER: US/0
FILING DATE: 08-JAN-1993
CLASSIFICATION: 514
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                                                COUNTRY: 1111A018

ZIP: 60606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN DATA:
SOFTWARE: PatentIN DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIPICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CLASSIPICATION: 514
ATTORNEY/AGENT INFORMATION:
NAMME: NO. 5604201nan, Kevin E
REGISTRATION NUMBER: 92,448
TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1000
TELERX: 910-221-5317
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: Amino acids
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Sequence 1, Application US/09023339

Sequence 1, Application US/09023339

FREEL NO. 6127145

GENERAL INFORMATION:

APPLICANT: Sutliff, Thomas D.

APPLICANT: Rodriguez, Raymond L.

TILLE OF INVENTION: Production of '1-Antitrypsin'

TITLE OF INVENTION: In Plants

NUMBER OF SEQUENCES: 22
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10 South Wacker Drive, Suite 3000
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Matches 390; Conservative
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MOLECULE TYPE: protein

US-08-002-202-6
                   Chicago
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61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: 1DT CO
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CLONE: mature AAT amino acid sequence
                                                 & Associates
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                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                            ADDRESSEE: Dehlinger & STREET: P.O. Box 60850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
CORRESPONDENCE ADDRESS:
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                                                                                                                                Palo Alto
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US-08-121-714-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-023-339-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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181 VFALVNYIFFKGKWERPFEVKDTEBEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
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                                                                                                                                                                                             APPLICANT: Sager, Ruth
APPLICANT: Zou, Zhiqiang
APPLICANT: Zou, Zhiqiang
APPLICANT: Anisowicz, Anthony
IITLE OF INVENTION: WASPIN, A NOVEL SERPIN WITH
IITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SITE: MASSACHESEUS
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DGG (Version 5.0)
SOFTWARE: WORDPETECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/47,108A
FILING DATE: June 7, 1995
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: 07/918,823
APPLICATION NUMBER: 07/918,296
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
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R: 06570/002002
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                                                                                                                    Sequence 3, Application US/08477108A Patent No. 5801001 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617) 542-8906
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Best Local Similarity 98.5
Matches 388; Conservative
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TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear
US-08-477-108A-3
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                                                                                               US-08-477-108A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 VPALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.6%; Score 2003; DB 1; 98.5%; Pred. No. 3.9e-181;
                       TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                                                                                                                                                                CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordeperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLAIMS TAIL

CLAIMS TAIL

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/938,823

APPLICATION NUMBER: 07/938,823

APPLICATION NUMBER: 07/844,296

FILING DATE: 02/28/92

APPLICATION NUMBER: 07/62,216

ATTORNEY/AGENT INFORMATION:

REGISTRATION NUMBER: 34,819

REGISTRATION NUMBER: 34,819

REGISTRATION NUMBER: 34,819

REGISTRATION NUMBER: 34,819

RELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFRAX: 617) 542-8906
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                                                                                                                            Fish & Richardson
                                                                                                                                                 STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 388; Conservative
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US-08-121-714-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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145 SEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDT 204
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                                                                                                                                                                                                                                                                            241 LMKYLGNATAIFFLPDEGKLOHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
                                                                                                                                                                                                                                                                                                    265 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 324
                                                                                                                                                                                                                                                                                                                                                                     301 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI 360
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  61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120
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                                             85 FAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10030330
; Patent No. 6833262
; GENERAL INFORMATION:
; APPLICANT: The University of Georgia Research Foundation, Inc
; TITLE OF INVENTION: A POLYPEPTIDE HAVING AMIDOLYTIC ACTIVITY FOR A SERPIN
; FILE REFERENCE: 235.00210201
; CURRENT APPLICATION NUMBER: US/10/030,330
; CURRENT PILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/130,436
; PRIOR FILING DATE: 1999-04-21
                                                                                                                                                                                                                                                                                                                                                                                                325 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI
                                                                                                                                                                                    181 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
LENGTH: 418
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ORGANISM: Homo sapiens
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                                                                                                                                 205 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKL,SSWVL 264
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08477112
; Patent No. 5905023
; GENERAL INFORMATION:
; TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
; TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
; VORRESPONDENCE 3, 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson P.C.
; STREET: 425 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 98.6%; Score 2003; DB 2; Best Local Similarity 98.5%; Pred. No. 3.9e-181; Matches 388; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                       385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTOK 418
                                                                                                                                                                                                                            361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDLUM TYPE: 3.5." Diskette, 1.44 Mb
MEDLUM TYPE: 3.5." Diskette, 1.44 Mb
MEDLUM TYPE: 3.5." Diskette, 1.44 Mb
COMPUTER: 1BM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
APPLICATION DATA:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/121,714
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/84,296
FILING DATE: 02/28/91
APPLICATION NUMBER: 07/862,216
APPLICATION NUMBER: 07/862,216
APPLICATION NUMBER: 34,819
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
TELEPAX: 06175
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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CITY: Boston
STATE: Massach
COUNTRY: U.S.A.
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181 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
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265 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 324
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APPLICANT: Benjanio, Stephane

APPLICANT: Benjanio, Hiroaki

TILE OF INVENTION: HUMAN CONAS AND PROTEINS AND USES THEREOF

FILE REPERBACE: 91.USG.DIV

CURRENT APPLICATION HUMBER: US/10/000,489

CURRENT APPLICATION NUMBER: US/10/000,489

CURRENT APPLICATION NUMBER: US 09/924,340

PRIOR FILING DATE: 2001-11-14

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-08-06

PRIOR FILING DATE: 2001-07-13

PRIOR PILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR FILING DATE: 2001-06-29

PRIOR PLING DATE: 2001-06-29

PRIOR PLING DATE: 2001-06-25

NUMBER OF SEQ ID NOS: 112

SOPTWARR: JEACHT

SEQ ID NO 92

LENGTH: 418

**WINDER OF SEQ ID NOS: 112

LENGTH: 418
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                                                                                                                                      PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                                                                                                                                                              385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418
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; Patent No. 6794363
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Best Local Similarity 98.0
Matches 386; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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; LOCATION: 1..24
US-10-000-489-92
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                                                                                                                                                                                                   APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES:
ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FAMLSLGTKADTHDEILEGINFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120
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98.6%; Score 2003; DB 5; Length 418;
Best Local Similarity 98.5%; Pred. No. 3.9e-181;
Matches 388; Conservative 3; Mismatches 3; Indels
                                     385 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418
                                                                                                                                                                                                                                                                                                                                                                                                      CORPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 553X
OPERATING SYSTEM: MS-DOS (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/91
ATTORNEY/ASTATION NUMBER: 07/662,216
ATTORNEY/ASTATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 34,819
REGISTRATION NUMBER: 0630/072001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1542-5070
TELEFAX: 6617) 542-8906
                                                                                                                                                           Sequence 3, Application PC/TUS9308322 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
PCT-US93-08322-3
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301 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI 360 120 240 181 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240 61 FAMISLGTKADTHDEILEGINPNIJQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120 121 SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180 121 SEGIKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDT 180 241 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300 241 LMKYLGNATAIFFLPDEGKLOHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300 1 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA 60 61 FAMLSVGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLHTLNQPDSQLQLTTGNGLFL 1 EDPOGDAAOKTDTSHHDODHPTFNKITPNLAEFAFSLYROLAHOSNSTNIFFSPVSIATA 181 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 301 SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI Gaps ö Length 394; Indels and Reagents for Inhibiting COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/002,202
FILING DATE: 08-JAN-1993
CCLASSIFICATION: 514
CCLASSIFICATION: 514 Score 1992; DB 2; Pred. No. 3.9e-180; 5; Mismatches 4; 361 PPEVKFNKPFVFLMIDQNTKSPLFMGKVVNPTQK 394 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394 ADDRESSEE: Allegretti and Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
STATE: 111inois
COUNTRY: USA Sequence 19, Application US/08002202; Sequence 19, Application US/08002202; Patent No. 5604201; GENERAL INFORMATION: APPLICANT: Thomas, Garry APPLICANT: Thomas, Laurel APPLICANT: Thomas, Laurel APPLICANT: Hayflick, Joel STITLE OF INVENTION: Methods and Reagents TITLE OF INVENTION: Methods and Reagents COMMESONERSONDENCE ADDRESS: ADDRESSES: ADDRESSES: ADDRESSES: ALLGOPATION: ALLGO ATTORNEY/AGENT INFORMATION:
NAME: No. 5604201nan, Kevin E
REGISTRATION NUMBER: 35,30003
REFERENCE/DOCKET NUMBER: 92,448 TELECOMMUNICATION INFORMATION TELEPHONE: 312-715-1000 TELEFAX: 312-715-1234 98.0%; Query Match
Best Local Similarity 97.7
Matches 385, Conservative TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS: 90909 US-08-002-202-19 RESULT 15

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SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180
                                                                                                                                                                  141 SEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTÇGKIVDLVKELDRDT 200
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                                                                                             EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
                                                                    Gaps
                                                                    4;
                                                   Length 414;
                                                                   2; Indels
                                                 Query Match
97.1%; Score 1973; DB 1;
Best Local Similarity 97.5%; Pred. No. 2.7e-178;
Matches 384; Conservative 4; Mismatches 2;
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Job time : 46 secs
LENGTH: 414 amino acids
; LENGTH: 414 amino aci
; TYPE: amino acid
; TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-002-202-19
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US-10-411-037-22
US-10-411-026-22
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US-10-411-049-22
US-10-411-012-22
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US-10-287-994-22
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Maximum Match 100%
Listing first 100 summaries
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Gapop 10.0 , Gapext 0.5
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Sequence 1219, Ap Sequence 1220, Ap Sequence 1222, App Sequence 122, App Sequence 23, App Sequence 24, App Sequence 27, App Sequence 29, App Sequence 29, App Sequence 20, App Sequence 20, App Sequence 50, App Sequence 21, App S Sequence 22, Appl Sequence 22, Appl Sequence 12, Appl Sequence 22, Appl Sequence 22, Appl Sequence 14, Appl Sequence 14, Appl Sequence 10, Appl Sequence 20, Appl Sequence 2304, Appl Sequence 2304, Appl Sequence 2304, Appl Sequence 2314, Appl Sequence 2314, Appl Sequence 1216, Appl Sequence 1219, Appl Sequence 1251, Ap Sequence 186, App Sequence 200, App Sequence 1380, Ap Sequence 1247, Ap 6 US-10-410-913-22
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7 US-10-410-980-22
7 US-10-410-980-22
7 US-10-410-980-22
7 US-10-410-897-22
7 US-10-410-897-22
7 US-10-410-897-22
7 US-10-410-410-4897-22
8 US-10-025-514-19
8 US-10-029-22-000-92
8 US-10-029-23-19
8 US-10-029-23-19
8 US-10-029-23-19
9 US-10-029-1665.5 1665.5 1665.5 1665.5 1665.5 1665.5 1665.5 1298 1282.5 1144.5 1122

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360
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                                                                                                      Sequence 2, Application US/10914863
; Sequence 2, Application US/10914863
; Publication No. US20050084972A1
; GENERAL INFORMATION:
; APPLICANT: BARR, PHILIP J.
; APPLICANT: GIBSON, HELEN L.
; TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST FILE REFERENCE: 3042-0012
; CURRENT FILING DATE: 2004-08-09
; PRIOR APPLICATION NUMBER: 60/493,984
; PRIOR FILING DATE: 2003-08-08
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 2.
                  361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                                 361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOHN MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                        RESULT 2
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; Sequence 2, Application US/10025514
; Publication No.
; GENERAL INFORMATION:
; APPLICANT: Hilip J. BARR
; APPLICANT: Hilip J. BARR
; APPLICANT: Philip FERBERTON
; TITLE OF INVENTION: MULTIFUNCTIONAL PROTEASE INHIBITORS AND
; TITLE OF INVENTION: THEIR USE IN TREATMENT OF DISEASE
; FILE REFERENCE: 368292000200
; CURRENT APPLICATION NUMBER: US/10/025,514
; CURRENT FILING DATE: 2002-14-03
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR APPLICATION NUMBER: U.S. 60/256,699
; PRIOR PILING DATE: 2001-11-20
; WUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 98.6%; Score 2003; DB 14; Length 394; Best Local Similarity 98.5%; Pred. No. 2.5e-154; Matches 388; Conservative 3; Mismatches 3; Indels 0
US-09-978-418-14
US-10-485-2211-14
US-10-485-2211-14
US-10-741-600-1212
US-10-741-600-1213
US-10-741-600-1213
US-10-741-600-1213
US-10-741-600-1215
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US-10-10-172-124
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US-10-10-172-139
US-10-210-172-130
US-10-210-172-130
US-10-210-172-130
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ORGANISM: Homo sapiens
               SEQ ID NO 2
LENGTH: 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-025-514-2
               181
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                                                                                     APPLICANT: Gordon B. WILLS

APPLICANT: Gordon B. WILLS

APPLICANT: Gordon B. WILLS

APPLICANT: Raren LU

APPLICANT: Raren LU

APPLICANT: Karen LU

APPLICANT: Karen LU

APPLICANT: Karen GLAT

APPLICANT: Xumei ZHAO

APPLICANT: Xumei ZHAO

APPLICANT: Xumei ZHAO

APPLICANT: Assen GLATT

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,

TITLE OF INVENTION: NUCLEIC Acid Molecules and Therapy of Ovarian Cancer

TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer

TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer

CURRENT FILING DATE: 2002-03-14

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-16

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-26

PRIOR FILING DATE: 2001-09-19

PRIOR FILING DATE: 2001-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LMKYLGNATAIPFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                         Peter VEIBY
Gordon B. MILLS
Robert C. BAST, Jr.
Rachel E. MEYERS
Michael MORRISEY
Peter OLANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-097-340-286
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APPLICANT:
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RESULT 4 US-10-411-037-22

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APPLICANT: Necus technical-set, and.
APPLICANT: Deprese, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer: Robert
APPLICANT: Bayer: Robert
APPLICANT: Bayer: Robert
APPLICANT: Bayer: Robert
APPLICANT: Bayer: Caryn
APPLICANT: Bower: Caryn
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
TITLE OF INVENTION: ALPHA GALACTOSIDASE A
FILE REPERBACE: 04085-01-5082
CURRENT FILING DATE: 2001-10-19
PRIOR PLILING DATE: 2001-10-19
PRIOR PLILING DATE: 2001-10-19
PRIOR PLILING DATE: 2002-06-07
PRIOR PLILING DATE: 2002-06-07
PRIOR PLILING DATE: 2002-06-07
PRIOR PLILING DATE: 2002-06-07
PRIOR PLILING DATE: 2002-08-16
PRIOR PLILING DATE: 2002-08-16
PRIOR PLILING DATE: 2002-09-16
PRIOR PLILING DATE: 2002-09-18
PRIOR PLILING DATE: 2002-09-18
PRIOR PLILIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEVKFNKPFVFLMIEONTKSPLFMGKVVNPTQK 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
Sequence 22, Application US/10411037
Publication No. US20040043446A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 22, Application US/10411026
                                                                                                                                           APPLICANT: Neose Technologies, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tryPE: PRT
CORGANISM: Homo sapiens
US-10-411-037-22
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US-10-411-026-22
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## APPLICANT: Hakes, uavid

APPLICANT: Hakes, uavid

APPLICANT: Chen, Xi

APPLICANT: Bowe, Caryn

ITILE OF INVENTION: GRANULCCTTE COLONY STIMULATING FACTOR: REMODELING AND

ITILE OF INVENTION: GLYOUNGATION OF G-CSF

TILLE OF INVENTION: GLYOUNGATION OF G-CSF

CURRENT APPLICATION NUMBER: US 60/328,523

PRIOR FILING DATE: 2001-10-10

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2001-10-19

PRIOR FILING DATE: 2002-06-07

PRIOR PILING DATE: 2002-06-07

PRIOR PLING DATE: 2002-06-07

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR APPLICATION NUMBER: US 60/391,777

PRIOR PILING DATE: 2002-06-16

PRIOR PILING DATE: 2002-06-25

PRIOR PRILING DATE: 2002-06-26

PRIOR PRILING DATE: 2002-06-26

PRIOR PILING DATE: 2002-06-26

PRIOR PILING DATE: 2002-06-26

PRIOR PILING DATE: 2002-06-26

PRIOR PILING DATE: 2002-08-16

PRIOR PILING DATE: 2002-08-18

PRIOR PILING DATE:
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Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418
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                                  Neose Technologies, Inc.
                                                              Defrees, Shawn
Zopf, David
Bayer, Robert
Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-410-962-22
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Publication No. US20040063911A1
GENERAL INFORMATION:
APPLICANT: Noese Technologies, Inc.
APPLICANT: DeFrees, Sham
APPLICANT: DeFrees, Sham
APPLICANT: DeFrees, Sham
APPLICANT: ARSPECTION: Robert
APPLICANT: ARSPECTION: Robert
APPLICANT: Chen, Xi
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION: METHODS
TITLE OF INVENTION WIMBER: US 60/328,523
FRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR APPLICATION NUMBER: US 60/344,692
PRIOR PLILNG DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR PRIOR PLILNG DATE: 2002-06-16
PRIOR PRIOR PLILNG DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
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Pred. No. 2.8e-154;
3; Mismatches 3; Indels 0
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US-10-410-962-22
Sequence 22, Application US/10410962
Publication No. US20040077836A1
GENERAL INFORMATION:
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Best Local Similarity 98.5
Matches 388; Conservative
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CORGANISM: Homo sapiens
US-10-411-026-22
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APPLICANT: BAYER, KOLLEL
APPLICANT: BAYER, KOLLEL
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: BAYER, CATT
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON
TITLE OF INVENTION: BETA
CURRENT APPLICATION NUMBER: US 60/328,523
FRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR PRILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR FILING DATE: 2002-06-07
PRIOR PRILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-07-17
PRIOR PRILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 98.6%; Score 2003; DB 16; Best Local Similarity 98.5%; Pred. No. 2.8e-154; Matches 388; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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APPLICANT: Neose Technologies, Inc.; APPLICANT: DeFrees, Shawn; APPLICANT: Zopf, David
Zopf, David
Bayer, Robert
Hakes, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-410-930-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-410-997-22
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                                                      APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONUGATION OF INTERFERON
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA
TITLE OF INVENTION: ALPHA
TILL OF INVENTION NUMBER: US 60/328,523
PRIOR FILLING DATE: 2001-10-19
PRIOR FILLING DATE: 2001-10-19
PRIOR FILLING DATE: 2002-06-07
PRIOR FILLING DATE: 2002-06-07
PRIOR FILLING DATE: 2002-07-17
PRIOR FILLING DATE: 2002-08-16
PRIOR FILLING DATE: 2002-08-18
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Pred. No. 2.8e-154;
3; Mismatches 3;
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; Sequence 22, Application US/10410930
; Publication No. US20040115168A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: DeFrees, Shawn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.64;
DeFrees, Shawn
Zopf, David
Bayer, Robert
Hakes, David
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Best Local Similarity 98.5
Matches 388; Conservative
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; ORGANISM: Homo sapiens
US-10-411-049-22
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APPLICANT: Hakes, David
APPLICANT: Hakes, Loavid
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryne
TITLE OF INVENTION: GLYCOBEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
TITLE OF INVENTION: METHODS
FILE REPRENCE: 040853-01-5031
CURRENT APPLICATION NUMBER: US 60/328,523
FRIOR PELING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-07
PRIOR FILING DATE: 2002-06-16
PRIOR FILING DATE: 2002-06-16
PRIOR PELING DATE: 2002-06-16
PRIOR PELING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PARENTIN VERSION 3.2
SOFTWARE: PARENTIN VERSION 3.2
SEQ ID NO 22
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; Publication No. US20040137557A1
; GENERAL INPORMATION:
A APPLICANT: Neose Technologies, Inc.
A APPLICANT: DeFrees, Shawn
; APPLICANT: Bayer, Robert
; APPLICANT: Bayer, Robert
; APPLICANT: Bowe, Caryn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
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                                                                APPLICANT: Bowe, Cary

APPLICANT: Bowe, Cary

TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF

TITLE OF INVENTION: FSH

TITLE OF INVENTION: FSH

TITLE OF INVENTION: FSH

TITLE OF INVENTION: FSH

CURRENT APPLICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/328,523

PRIOR APPLICATION NUMBER: US 60/344,692

PRIOR PILING DATE: 2001-10-19

PRIOR FILING DATE: 2002-06-07

PRIOR PILING DATE: 2002-06-07

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-06-15

PRIOR PILING DATE: 2002-08-16

PRIOR FILING DATE: 2002-08-16

PRIOR PILING DA
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GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc., APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Reyer, Robert
                     Hakes, David
Chen, Xi
Bowe, Caryn
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; ORGANISM: Homb sapiens
US-10-410-997-22
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TLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES
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Pred. No. 2.8e-154;
3; Mismatches 3;
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          TITLE REFERENCE: 040853-01-5052-00
CURRENT APPLICATION NUMBER: US/10/287,994
CURRENT PILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-10-19
PRIOR FILING DATE: 2001-0-19
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-25
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-08-16
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-18
PRIOR FILING DATE: 2002-08-28
NUMBER OF SEQ ID NOS: 62
SOFTWARE: PATENTIN VERSION 3.1
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Publication No. US20040142856A1
GENERAL INPORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Hakes, David
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
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; ORGANISM: Homo sapiens
US-10-287-994-22
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Best Local Similarity
Matches 388; Conserv
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US-10-410-913-22
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TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS
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APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryn
TITLE OF INVENTION: INTERLEUKIN-2: REMODELING AND GLYCOCONJUGATION OF IL-2
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                                                        TITLE DOF INVESTION: METHOUS:
CURRENT APPLICATION NUMBER: US/10/410,913
CURRENT FILING DATE: 2003-04-09
PRIOR PLLING DATE: 2003-04-09
PRIOR PLLING DATE: 2001-10-10
PRIOR PLLING DATE: 2001-10-19
PRIOR PLLING DATE: 2001-10-19
PRIOR PLLING DATE: 2001-019
PRIOR PLLING DATE: 2002-06-07
PRIOR PLLING DATE: 2002-06-07
PRIOR PLLING DATE: 2002-06-07
PRIOR PLLING DATE: 2002-06-25
PRIOR PLLING DATE: 2002-06-25
PRIOR PLLING DATE: 2002-06-25
PRIOR APPLICATION NUMBER: US 60/396,594
PRIOR PLLING DATE: 2002-06-25
PRIOR PLLING DATE: 2002-06-16
PRIOR PLLING DATE: 2002-08-16
PRIOR PLLING DATE: 2002-08-18
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APPLICANT: Neose Technologies, Inc.; APPLICANT: DeFrees, Shawn; APPLICANT: Zopf, David; APPLICANT: Hayes, David; APPLICANT: Chen, Xi APPLICANT: Chen, Xi APPLICANT: Bowe, Caryn
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ORGANISM: Homo sapiens
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US-10-971-461-15
is Sequence 15, Application US/10971461
is Publication No. US20050070477A1
is GENERAL INFORMATION:
is APPLICANT: Cochrane, Charles G.
is APPLICANT: The Scripps Research Institute
is FILE REFERENCE: 1361.037US1
is FILE REFERENCE: 1361.037US1
is CURRENT APPLICATION NUMBER: US/10/971,461
is CURRENT FILING DATE: 2004-10-22
is NUMBER OF SEQ ID NOS: 30
is SOFTWARE: FastSEQ for Windows Version 4.0
is SEQ ID NO 15
is LENGTH: 418
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Best Local Similarity 98.5%; Pred. No. 2.8e-154;
Matches 388; Conservative 3; Mismatches 3;
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             CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US(10/410,980
PRIOR APPLICATION NUMBER: US 60/328,523
PRIOR PLING DATE: 2001-10-10
PRIOR PLLING DATE: 2001-10-19
PRIOR PELING DATE: 2001-01-9
PRIOR PELING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: US 60/391,777
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-25
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-16
PRIOR PELING DATE: 2002-08-18
FILE REFERENCE: 040853-01-5066
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US-10-410-980-22
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APPLICANT: ROBER SECULIOLISTICS AND APPLICANT: SOBE SECULIONS APPLICANT: BAYER, SOBERT APPLICANT: BAYER, ROBERT APPLICANT: BAYER, ROBERT APPLICANT: BAYER, DAVID APPLICANT: BAYER, DAVID APPLICANT: BAYER, DAVID APPLICANT: BAYER, DAVID APPLICANT: BAYER, Chen, Xi APPLICANT: BAYER, Chen, Xi APPLICANT: BAYER, CHEN, Xi APPLICANT: BAYER, COLONDUGATION OF FACTOR IX, FILE OF INVENTION: FACTOR IX, REWODELING AND GLYCOCCONJUGATION OF FACTOR IX, FILE REFERENCE: 040853-01-5058 (0/328,523)
FRIOR FILING DATE: 2003-04-09
FRIOR APPLICATION NUMBER: US 60/344,692
FRIOR PILING DATE: 2001-10-19
FRIOR PILING DATE: 2002-06-05
FRIOR PILING DATE: 2002-06-16
FRIOR PILING DATE: 2002-06-16
FRIOR PILING DATE: 2002-06-16
FRIOR PILING DATE: 2002-08-16
FRIOR PILING DATE: 2002-08
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                                                                                                                                      98.6%; Score 2003; DB 17;
98.5%; Pred. No. 2.8e-154;
tive 3; Mismatches 3;
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                                                                                                                                      Query Match
Best Local Similarity 98.5
Matches 388; Conservative
ORGANISM: Homo sapiens
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US-10-410-897-22

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VPALVNYIFFKGKWERPFEVKDTBEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
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                                                          1 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA 60
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Query Match 98.6%; Score 2003; DB 17; Length 418; Best Local Similarity 98.5%; Pred. No. 2.8e-154; Matches 388; Conservative 3; Mismatches 3; Indels 0
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                                                                                                                                                                              EDPQGDAAQKTDTSHHDQDH.....IEQNTKSPLFMGKVVNPTGK
                                                                                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                     6959266 seqs, 1168006243 residues
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries
                                                                   protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Sequence 2 Sequence 2 Sequence 2

Sequence

Sequence Sequence Sequence

Sequence 22, Appl Sequence 22, Appl Sequence 20, Appl Sequence 15, Appl Sequence 15, Appl Sequence 16, Appl Sequence 18, Appl Sequence 18, Appl Sequence 16, Appl Sequence 16, Appl Sequence 20, Appl Sequence 20, Appl Sequence 2304, Appl Sequence 1215, Appl Sequence 1215, Appl Sequence 1219, Appl Sequence 1221, Appl Sequence 1222, Appl Sequence 12222, Appl Sequence 1222, Appl Sequence 12222, Appl Sequ

Sequence 286, App Sequence 22, Appl Sequence 20, Appl Sequence 22, Appl Sequence 22, Appl Sequence 2, Appl Sequence 3, Appli Sequence 3, Appli Sequence 139167, Sequence 139167, Sequence 286, App Sequence 9476, Ap Sequence 9476, Ap Sequence 22, Appl Sequence 22, Appl

Sequence 9, A Sequence 6, A Sequence 1, A Sequence 1, A Sequence 6, A Sequence 2, A Se

Description

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Sequence 28 Sequence 28 Sequence 22

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 11592, Sequence 1216, Ag Sequence 1216, Ag Sequence 1217, Ar

US-10-170-205E-19559 US-10-219-051B-6542 US-10-219-051B-11592 US-10-741-600-1216 US-10-741-600-1217

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pdx1.rapm

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Sequence 6, Application US/09290034C
; Sequence 6, Application US/09290034C
; GENERAL INFORMATION:
; APPLICANT: Jean, Francois
; APPLICANT: Thomas, Gary
; TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 9448-H
; CURRENT APPLICATION NUMBER: US/09/290,034C
; CURRENT PILING DATE: 1999-04-08
; PRIOR APPLICATION NUMBER: 60/081,034
; PRIOR FILING DATE: 1998-04-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-290-034C-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180
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                                                                                                                                                                                                                                                                                     /label=Variant
/ note="The amino acid sequence is the amino acid
sequence of the modified alpha-1-antitrypsin
protein, alpha-1-antitrypsin Portland."
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MOLECULE TYPE: protein
FRAURE:
NAME/KEY: Modified site
LOCATION: 355.358
OTHER INFORMATION: /label=
OTHER INFORMATION: /cotein
CTHER INFORMATION: sequenc
CTHER INFORMATION: protein
US-09-372-003-9
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INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
    TELEPHONE: 312-913-0001
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                        TELEFAX: 312-913-0002
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US-09-290-034C-6
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GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Nelson, Jay
APPLICANT: Nelson, Jay
APPLICANT: Renglen, Stephan G
TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin
TITLE OF INVENTION: Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
FILING DATE:
CLASSIFICATION:
US-10-741-600-1218

US-10-741-600-1219

US-10-741-600-1220

US-10-741-600-1222

US-10-741-600-1222

US-10-995-561-753

US-10-995-561-754

US-10-995-561-756

US-10-995-561-756

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US-10-995-561-757

US-10-995-561-759

US-10-995-759

US-10-995

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300 South Wacker Drive
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US-60-608-498-721
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REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 92,448-D
TELECOMMUNICATION INPORMATION:
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APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
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Length 394; DB 16; 99.7%; Score 2026;

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LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRATURE:
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Best Local Similarity 99.5%;
Matches 392; Conservative
                                                                                                                     NAME/KEY: Modified site
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ORGANISM: Homo sapiens
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                                                         EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
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GENERAL INFORMATION:
APPLICANT: Thomas, Gary
APPLICANT: Thomas, Laurel
APPLICANT: Homas, Laurel
APPLICANT: Nelson, Jay
APPLICANT: Stenglen, Stephan G
ITILE OP INVENTION: Endoprotease
ITILE OP INVENTION: Endoprotease
WUMBER OF SEQUENCES: 21
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                     Indels
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300 South Wacker Drive
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
 Pred. No. 1.4e-176;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361 PPEVKENKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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REFERENCE/DOCKET NUMBER: 92,448-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-SEP-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
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Best Local Similarity 99.7%;
Matches 393; Conservative
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REGISTRATION NUMBER: 3
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STREET: 30
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US-09-372-003-11
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GENERAL INFORMATION:
APPLICANT: Jean, Francois
APPLICANT: Thomas, Gary
TITLE OF INVENTION: Reagents and Methods for Inhibiting Furin Endoprotease
TITLE OF INVENTION: Activity
FILE REPERBNCE: 92448-H
CURRENT APPLICATION NUMBER: US/09/290,034C
CURRENT FILING DATE: 1999-04-08
PRIOR PILING DATE: 1998-04-09
PRIOR FILING DATE: 1998-04-09
                                                                                                                                                                                                                                                                                                                                                                                          1 EDPQGDAAQKIDISHHDQDHPIFNKIIPNLAEFAFSLYRQLAHQSNSINIFFSPVSIATA 60
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LOCATION: 355.358
COTHER INFORMATION: /label=Variant
COTHER INFORMATION: / note="The amino acid sequence is the amino OTHER INFORMATION: gequence of the modified alpha-1-antitrypsin cother InfoRMATION: protein, alpha-1-antitrypsin pittsburgh."
US-09-372-003-11
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                                                                                                                                                                                                                               Length 394;
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                                                                                                                                                                                                                         Query Match 99.7%; Score 2026; DB 17; Best Local Similarity 99.7%; Pred. No. 1.4e-176; Matches 393; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2021; DB 16;
Pred. No. 4.1e-176;
0; Mismatches 2;
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Query Match
Best Local Similarity 99.5
Matches 392; Conservative
      MOLECULE TYPE: protein
               7 MOLECULE 13
US-09-372-003-6
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                                                                                                                            61 PAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFOELLRTLNQPDSQLOLTTGNGLFL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reagents for Inhibiting Furin
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/372,003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/481,534
FILING DATE: 14-5EP-1995
ATTORNEY/AGENT INFORMATION:
NAME: NGORAN, KEVIN E
REGISTRATION NUMBER: 35.303
REFERENCE/DOCKET NUMBER: 92,448-D
TELECOMMUNICATION:
TELEPHONE: 312-913.0001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09372003
Sequence 6, Application US/09372003
GENERAL INFORMATION:
APPLICANT: Thomas, Exic D
APPLICANT: Thomas, Laurel
APPLICANT: Hayflick, Joel S
APPLICANT: Hayflick, Joel S
APPLICANT: Stenglen, Stephan G
TITLE OF INVENTION: Methods and Rea
TITLE OF INVENTION: Endoprotease
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES:
ADD
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SEQUENCE CHARACTERISTICS:
LENGTH: 394 amino acids
TYPE: amino acid
TOPOLOGY: linear
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ó 61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120 61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120 121 SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180 180 181 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240 61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120 121 SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 180 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300 9 9 9 1 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEPAFSLYRQLAHQSNSTNIFFSPVSIATA 121 SQGLKLVDKFLEDVKKLYHSEAFTVNFGDTEQAKKQINDYVEKGTQGKIVDLVKELDRDT 241 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 61 FAMLSLGTKADTHDEILLEGLNFNLTEIPEAQIHEGFQELLKTLNQPDSQLQLTTGNGLFL 181 VPALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 1 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA Gaps Gaps ö ö US-10-162-184-2.
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US-10-18-2.
US-10-2.
US Length 394; Length 394; Indels Indels Query Match 98.6%; Score 2003; DB 26; Best Local Similarity 98.5%; Pred. No. 1.9e-174; Matches 388; Conservative 3; Mismatches 3; 99.4%; Score 2020; DB 17; 99.5%; Pred. No. 5.1e-176; cive 0; Mismatches 2; 361 PPEVKFNKPFVFLMIEONTKSPLFMGKVVNPTGK 394

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FULT-UNIAL-07826-286, Application PC/TUS0207826

GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc. et al.
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Nucleic Acid Molecules and Therapy of Ovarian Cancer
FILE REFERENCE: MI-030PC
CURRENT APPLICATION NUMBER: 60/276,025
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-09-27
PRIOR PLING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 60/326,149
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-16
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: PESESEQ for Windows Version 4.0
SEQ ID NO 286
LENGTH: 418
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Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3;
       PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 395
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; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
PCT-US02-07826-286
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                                                                                                                                                                                                                                                                                          SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: amino acid sequence OTHER INFORMATION: encoded by rAAT expression plasmid pyEP829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VFALVNYIFFKGKWERPFEVKDIEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVLGQLGITKVFSNGADLSGVTEBAPLKLSKAVHKAVLTIDEKGTBAAGAMFLERIPRSI 360
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SEGLKLYDKFLEDVKKLYHSEAFTYNFGDTEEAKKQINDYVEKGTGGKIYDLVKELDRDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/10914863
GENERAL INFORMATION:
APPLICANT: BARR, PHILIP J.
TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST
TITLE OF INVENTION: METHODS OF PROTEIN PRODUCTION IN YEAST
FILE REFERENCE: 39042-0012
CURRENT APPLICATION NUMBER: US/10/914,863
CURRENT PILING DATE: 2004-08-09
PRIOR APPLICATION NUMBER: 60/493,984
PRIOR APPLICATION NUMBER: 60/493,984
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 3.2
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Pred. No. 1.9e-174;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                          361 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394
                                                                                                                                                                                                                                                                                                                                                                                     PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 394
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TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 98.5
Matches 388; Conservative
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PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 418
                                                                                            PCT-US03-12324-20; Sequence 20, Application PC/TUS0312324; GENERAL INFORMATION:
             385
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PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTGK 394

361

181

121

241

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APPLICANT: FIGURE R.

APPLICANT: SONG, SIHONG
APPLICANT: SONG, SIHONG
APPLICANT: SONG, SIHONG
APPLICANT: SONG, SIHONG
APPLICANT: LOILER, SCOTT A.

TITLE OF INVENTION: TRAX VECTOR-BASED COMPOSITIONS AND METHODS FOR THE PREVENTION AND
TITLE OF INVENTION: TRAX VECTOR-BASED COMPOSITIONS AND METHODS FOR THE PREVENTION AND AND
TITLE OF INVENTION: TRAX VECTOR-BASED COMPOSITIONS FOR THE PREVENTION AND AND
TITLE OF INVENTION: TRAX VECTOR-BASED COMPOSITIONS FOR THE PREVENTION AND AND
TITLE OF INVENTION NUMBER: POT/US03/12324
CURRENT APPLICATION NUMBER: 60/374,083
PRIOR APPLICATION NUMBER: 60/374,083
PRIOR APPLICATION NUMBER: 60/374,083
PRIOR FILING DATE: 2003-04-19
NUMBER OF SEQ ID NOS: 54
SEQ ID NO 20
LENGTH: 418
TYPE: PRI HOMO SADIENS
PCT-US03-12324-20
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APPLICANT: The Scripps Research Institute
APPLICANT: Cochrane, Charles G.
APPLICANT: Oches, Zenaida G.
APPLICANT: Oches, Zenaida G.
APPLICANT: Revak, Susan D.
APPLICANT: Niven, Ralph
TITLE OF INVENTION: Treatment and Prevention of Pulmonary Conditions
FILE REFERENCE: 1361.037W01
CURRENT FILING DATE: 2003-04-25
PRIOR PLICATION NUMBER: US 60/375,968
PRIOR FILING DATE: 2003-04-25
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 418
TYPE: PRT
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Pred. No. 2.1e-174;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.5%;
Matches 388; Conservative
                    ATKINSON, MARK
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APPLICANT: 20Pf, David
APPLICANT: 20Pf, David
APPLICANT: Bower, Robert
APPLICANT: Bower, Caryn
APPLICANT: Bower, Caryn
APPLICANT: Bower, Caryn
APPLICANT: Bower, Caryn
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
TITLE OF INVENTION: REMODELING AND GIYCOCONJUGATION OF PEPTIDES
TITLE PREPERRECE: 2002-10-50
CURRENT FILING DATE: 2002-10-31
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-10-19
PRIOR PILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR PILING DATE: 2001-11-08
PRIOR PILING DATE: 2002-10-334,301
PRIOR PILING DATE: 2002-10-6-25
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-07
PRIOR PILING DATE: 2002-06-17
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-16
PRIOR PILING DATE: 2002-08-18
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98.6%; Score 2003; DB 1; 98.5%; Pred. No. 2.1e-174; iive 3; Mismatches 3;

Query Match
Best Local Similarity 98.5
Matches 388; Conservative

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NUMBER OF SEQ ID NOS: 62 SOFTWARE: Patentin version 3.1

LENGTH: 418 TYPE: PRT ORGANISM: Homo sapiens

; UKGANISM: HOM PCT-US02-32263-22

9 84 180

204

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TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: GLYCOPEGYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE TITLE OF INVENTION: METHODS GREEN TO A METHODS GREEN TO A METHOD STATE TO A METHOD STATE TO A METHOD STATE TO A METHOD OF A STATE TO A METHOR TILING DATE: 2001-10-10 PRIOR PELICATION NUMBER: US 60/334,233
PRIOR PELING DATE: 2001-10-20
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PRIOR PELING DATE: 2001-10-19
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PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2001-10-19
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-07
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-17
PRIOR PELING DATE: 2002-06-18
PRIOR PELING DATE: 2002-06-
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Zopf, David
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APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryne
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LYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Derive, Sineman,
APPLICANT: Bayer, Robert
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Chen, Xi
APPLICANT: Bowe, Caryne
TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION: ERYTHROPOIETIN: REMODELING AND GLYCOCONJUGATION OF
TITLE OF INVENTION: ERYTHROPOIETIN:
FILE REFERENCE: 040853-01-5083WO
CURRENT FILING DATE: 2003-10-09
FRIOR FILING DATE: 2003-10-09
FRIOR FILING DATE: 2002-11-5
FRIOR FILING DATE: 2003-01-06
FRIOR FILING DATE: 2003-01-06
FRIOR FILING DATE: 2003-03-17
FRIOR FILING DATE: 2003-04-09
NUMBER OF SEQ ID NOS: 75
SUPPLARE: PatentIn version 3.2
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                                                                                         Length 418;
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                                                                                      Score 2003; DB 1;
Pred. No. 2.1e-174;
3; Mismatches 3;
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GENERAL INFORMATION:
APPLICANT: Neose Technologies, Inc.
APPLICANT: DeFrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Bayer, Robert
APPLICANT: Hakes, David
                                                                                   Query Match
Best Local Similarity 98.5%;
Matches 388; Conservative
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; ORGANISM: Homo sapiens
PCT-US03-12731-15
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Best Local Similarity
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PCT-US03-31974-22
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                                                                                                                                         25 EDPQGDAAQKTDTSHHDQDHPTFNKITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
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                                   98.6%; Score 2003; DB 1; Length 418; 98.5%; Pred. No. 2.1e-174; ive 3; Mismatches 3; Indels
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ZIP: 60606-4002
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Tilton, Fallon, Lungmus & Chestnut
100 South Wacker Drive - Suite 960
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GENERAL INFORMATION:
APPLICANT: Brigham, Kenneth
APPLICANT: Conary, Jon
APPLICANT: Canonico, Angelo
APPLICANT: Meyrick, Barbara
ITILE OF INVENTION: DNA Construct for
ITILE OF INVENTION: a Human Gene
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADRESS:
ADDRESSEE: Tilton, Fallon, Lungmus
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REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: VU9111
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PRIOR APPLICATION DATA.
APPLICATION NUMBER: US 690,283
FILING DATE: 24-APR-1991
ATTORNEY/AGENT INFORMATION:
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TELEPHONE: (312) 456-8000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                      Best Local Similarity 98. Matches 388; Conservative
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STATE: Illinois
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PCT-US04-11494-22
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US-08-459-292-2
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                                                                                                                                                                       Length 418;
                                                                                                                                                                                                                           Indels
                                                                                                                                                               Score 2003; DB 8;
Pred. No. 2.1e-174;
3; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.

ZITP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,758
FILING DATE:
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,714
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,236
APPLICATION NUMBER: 07/938,236
APPLICATION NUMBER: 07/938,236
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
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; Sequence 3, Application US/08472758
; GENERAL INFORMATION:
                                                                                                                                                                    Query Match
Best Local Similarity 98.5%;
Matches 388; Conservative
LENGTH: 418 amino acids
TYPE: amino acid
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-292-2
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98.6%; Score 2003; DB 8; Length 418;
Best Local Similarity 98.5%; Pred. No. 2.1e-174;
Matches 388; Conservative 3; Mismatches 3; Indels
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ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/POCKET NUMBER: 06570/002003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELERA: (617) 542-8906
TELERA: 200154
INPORMATION FOR SEQ ID NO: 3:
LENGTH: 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: June 20, 2005, 19:55:44 Job time : 492 secs
                                                                                                                                                                                                                  ; TYPE: amino acid; STRANDEDNESS: ; TOPOLOGY: linear US-08-472-758-3
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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747.214 Million cell updates/sec PDX1 2032 1 EDPQGDAAQKTDTSHHDQDH.....IEQNTKSPLFMGKVVNPTGK 394 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

583429 Total number of hits satisfying chosen parameters:

583429 seqs, 123271311 residues

Searched:

Post-processing: Minimum Match 10% Maximum Match 100% Listing first 100 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pending_Patents_AA_New:*

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2: /cgn2_6/ptodata/2/paa/USO6_NBW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/USO7_NBW_COMB.pep:*

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7: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

8: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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NUMBER OF SEQ ID NOS: 33
                SEQ ID NO 2
LENGTH: 394
TYPE: PRT
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APPLICANT:
APPLICANT:
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   Арр
Арр
                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Arrive PARATION:
APPLICANT: Arrive Pharmaceuticals, Inc.
APPLICANT: Arrive Pharmaceuticals, Inc.
TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
FILE REFERENCE: 35042-0020 PCT
CURRENT APPLICATION NUMBER: PCT/USO5/07959
CURRENT FILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-03-18
PRIOR FILING DATE: 2005-03-09
NUMBER OF SEQ ID NOS: 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EDPQGDAAQXTDTSHHDQDHPTFNXITPNLAEFAFSLYRQLAHQSNSTNIFFSPVSIATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/11077276
GENERAL INFORMATION:
BAPPLICANT: Philip J. BARR
APPLICANT: Philip DEMBERTON
APPLICANT: Philip DEMBERTON
APPLICANT: Helen GIBSON
ITILE OF INVENTION: TRRATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE ITILE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
FILE REFERENCE: 39042-0020
CURRENT APPLICATION NUMBER: US/11/077,276
CURRENT PILING DATE: 2005-03-09
PRIOR FILING DATE: 2005-03-09
PRIOR FILING DATE: 2004-03-09
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US-60-664-579-565
US-60-664-579-566
                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.5
Matches 388; Conservative
   415
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   23.7
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US-11-077-276-2
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APPLICANT: Kumei ZHAO
APPLICANT: Kumei ZHAO
APPLICANT: Kumei ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
TILE REPERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/11/050,926
CURRENT PILING DATE: 2005-02-04
PRIOR APPLICATION NUMBER: US/10/097,340
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR PILING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR APPLICATION NUMBER: 60/276,026
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PRIOR APPLICATION NUMBER: 60/276,026
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                                                                                     Query Match
98.6%; Score 2003; DB 7; Length 394;
Best Local Similarity 98.5%; Pred. No. 1.3e-149;
Matches 388; Conservative 3; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVARAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISEY
APPLICANT: Peter OLANDT
APPLICANT: Peter SEN
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Robert C. BAST, Jr.
Karen LU
Rosemarie SCHMANDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peter VEIBY
ORGANISM: Homo sapiens
US-11-077-276-2
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180 204

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APPLICANT: Raelson, John V
APPLICANT: Paquin, Bruno
APPLICANT: Paquin, Bruno
APPLICANT: Croteau, Pascal
APPLICANT: Little, Randall D
APPLICANT: Cousineau, Johanne
APPLICANT: Cousineau, Johanne
APPLICANT: Segal, Jonathan
TITLE OF INVENTION: GeneMap of the Human Genes Associated with Psoriasis
FILE REPERENCE: 059908-5005-R
CURRENT APPLICATION WINBER: US/60/685,372
CURRENT FILING DATE: 2005-05-31
NUMBER OF SEQ ID NOS: 2738
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1012
LENGTH: 418
                                                             85 PAMLSLGTKADTHDEILEGLNFNLTEIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 144
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                                                                                                                                                              145 SEGLKLVDKFLEDVKKLYHSEAFTVNFGDTEEAKKQINDYVEKGTQGKIVDLVKELDRDT
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                                      PAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL
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98.5%; Pred. No. 1.4e-149;
live 3; Mismatches 3;
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Best Local Similarity 98.5
Matches 388; Conservative
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; ORGANISM: Homo sapiens
US-60-685-372-1012
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GENERAL INFORMATION:
APPLICANT: JOSELOFF E 11 Cabeth et al.
TITLE OF INVENTION: LUNG DISEASE TARGETS AND USES THEREOF FILE REFERENCE: CL001602
CURRENT APLICATION NUMBER: US/60/680,004
CURRENT PILNG DATE: 2005-05-12
NUMBER OF SEQ ID NOS: 1729
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 418
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98.6%; Score 2003; DB 7;
Best Local Similarity 98.5%; Pred. No. 1.4e-149;
Matches 388; Conservative 3; Mismatches 3;
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PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR PILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR PILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 6/325,102
PRIOR PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-19
NUMBER: OF SEQ ID NOS: 363
SEQ ID NO 286
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Best Local Similarity 98.5
Matches 388; Conservative
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-050-926-286
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ORGANISM: Homo sapiens
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US-60-680-004-3
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APPLICANT: Belouch;
APPLICANT: Belouch;
APPLICANT: Bradley, Walter E
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APPLICANT: Bradley, Walter E
APPLICANT: Croteau, Pascal
APPLICANT: Croteau, Pascal
APPLICANT: Little, Randall D
APPLICANT: Little, Randall D
APPLICANT: Entdewegh, Paul V
APPLICANT: Berdewegh, Paul V
APPLICANT: Gesgal, Johanhan
APPLICANT: Gesgal, Johanhan
APPLICANT: Gesgal, Johanhan
APPLICANT: Gesgal, Johanhan
APPLICANT: Bergel, Baul V
APPLICANT: COURTION: GeneWap of the Human Genes Associated with Psoriasis
CURRENT APPLICATION NUMBER: US 60/685,372
CURRENT APPLICATION NUMBER: US 600-6931
NUMBER OF SEQ ID NOS: 2738
SEQ ID NOS: 2738
SEQ ID NO 1014
I.ENGTH. 418
LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
                     LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 324
                                                                      SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLERIPRSI 360
                                                                                           SVLGQLGITKVFSNGADLSGVTEEAPLKLSKAVHKAVLTIDEKGTEAAGAMFLEAIPMSI 384
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Pred. No. 1.4e-149;
3; Mismatches 3;
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Best Local Similarity 98.5%;
Matches 388; Conservative
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US-60-685-372-1014
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TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
FILE REFERENCE: 39042-0020 PCT
CURRENT APPLICATION NUMBER: PCT/USOS/07959
PRIOR APPLICATION NUMBER: U.S. 60/551,856
PRIOR APPLICATION NUMBER: U.S. 60/551,856
NUMBER OF SEQ ID NOS: 33
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APPLICANT: Bradley, Walter E
APPLICANT: Paquin, Bruno
APPLICANT: Oroteau, Pascal
APPLICANT: Allard, Rene
APPLICANT: Little, Randall D
APPLICANT: Little, Randall D
APPLICANT: Escadewegh, Paul V
APPLICANT: Segal, Jonanne
APPLICANT: Segal
APP
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Pred. No. 1.4e-149;
3; Mismatches 3;
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Sequence 1016, Application US/60685372 GENERAL INFORMATION:
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                                                                                                   APPLICANT: Belouchi, Abdelmajid
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98.5%;
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SOFTWARE: Patentin version 3.3
SEQ ID NO 1016
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Best Local Similarity 98.5
Matches 388; Conservative
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ORGANISM: Homo sapiens
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LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 300
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GENERAL INFORMATION:
APPLICANT: Philip J. BARR
APPLICANT: Philip DEMBERTON
APPLICANT: Philip DEMBERTON
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
TITLE OF INVENT APPLICATION NUMBER: US/11/077,276
CURRENT APPLICATION NUMBER: US. 60/551,856
PRIOR APPLICATION NUMBER: U.S. 60/551,856
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 8.
                                        182 VFALVNYIFFKGKWERPFEVKDTEEEDFHVDQVTTVKVPMMKRLGMFNIQHCKKLSSWVL
                                                                                                            242 IMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK
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Pred. No. 1.7e-149;
3; Mismatches 3;
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162 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 395
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Best Local Similarity 98.5%;
Matches 388; Conservative
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ORGANISM: Homo sapiens
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US-11-077-276-8
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TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE |
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
FILE REFERENCE: 39042-0020 PCT
CURRENT APPLICATION NUMBER: PCT/USOS/07959
CURRENT FILING DATE: 2005-03-18
PRIOR APPLICATION NUMBER: U.S. 60/551,856
PRIOR FILING DATE: 2004-03-09
NUMBER OF SEQ ID NOS: 33
SEQ ID NOS: 33
                                                                                                                                             Gaps
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                                                                                                          Length 503;
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Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3;
                                                                                                      Query Match

98.6%; Score 2003; DB 1;
Best Local Similarity 98.5%; Pred. No. 1.7e-149;
Matches 388; Conservative 3; Mismatches 3;
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TYPE: PRT
ORGANISM: Homo sapiens
                                  TYPE: PRT
ORGANISM: Homo sapiens
PCT-US05-07959-8
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PCT-US05-07959-16
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SEQ ID NO 8
LENGTH: 503
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98.6%; Score 2003; DB 1; Length 522;
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GENERAL INFORMATION:
BPPLICANT: Arriva Pharmaceuticals, Inc.
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
TITLE REPERBNCE: 39042-0020 PCT
CURRENT APPLICATION NUMBER: PCT/USOS/07959
CURRENT FILING DATE: 2005-031-18
PRIOR PILING DATE: 2005-031-18
PRIOR FILING DATE: 2004-03-09
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 20
LENGTH: 522
                                                                                                                                              FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL
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98.5%; Pred. No. 1.8e-149;
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Best Local Similarity 98.5%; Pred. No. 1.8e-149;
Matches 388; Conservative 3; Mismatches 3;
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                     388; Conservative
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ORGANISM: Homo sapiens
Best Local Similarity
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APPLICANT: ATTACKATION.
APPLICANT: ATTACKATION.
TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE ITILE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
FILE REPERENCE: 39042-0020 PCT
CURRENT APPLICATION NUMBER: PCT/USO5/07959
CURRENT APPLICATION NUMBER: DCT/USO5/07959
PRIOR APPLICATION NUMBER: U. S. 60/551,856
PRIOR FILING DATE: 2004-03-09
PRIOR FILING DATE: 2004-03-09
SEQ ID NO 14
LENGTH: 522
                                                        APPLICANT: Philip J. BARR
APPLICANT: Philip J. BARR
APPLICANT: Philip PEMBERTON
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
TITLE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
CURRENT APPLICATION UNMBER: US/11/077,276
CURRENT FILING DATE: 2005-03-09
PRIOR PRILING DATE: 2004-03-09
NUMBER OF SEQ ID NOS: 33
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98.5%; Pred. No. 1.7e-149;
tive 3; Mismatches 3;
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  US-11-077-276-16; Sequence 16, Application US/11077276; GENERAL INFORMATION:
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Best Local Similarity 98.5
Matches 388; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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PCT-US05-07959-14
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242 LMKYLGNATAIFFLPDEGKLQHLENELTHDIITKFLENEDRRSASLHLPKLSITGTYDLK 301
                                                        61 FAMLSLGTKADTHDEILEGLNFNLTQIPEAQIHEGFQELLRTLNQPDSQLQLTTGNGLFL 120
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US-11-077-276-20
; Sequence 20, Application US/11077276
; GENERAL INFORMATION:
; APPLICANT: Philip 7. BARR
; APPLICANT: Philip PEMBERTON
; APPLICANT: Helen GIBSON
; TITLE OF INVENTION: TREATMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE BY
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SEQUENCE 14, Application US/1107276

SEQUENCE INFORMATION:
APPLICANT: Philip J. BARR
APPLICANT: Philip DEMBERTON
APPLICANT: Helen GIBSON
TITLE OF INVENTION: TRAITMENT OF CHRONIC OBSTRUCTIVE PULMONARY DISEASE ITILE OF INVENTION: LOW DOSE INHALATION OF PROTEASE INHIBITOR
TITLE REFERENCE: 39042-0020
CURRENT PAPLICATION NUMBER: U.S. 10/51,956
PRIOR APPLICATION NUMBER: U.S. 60/551,856
PRIOR APPLICATION NUMBER: U.S. 60/551,856
NUMBER OF SEQ ID NOS: 33
SEQ ID NO 14
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Best Local Similarity 98.5%; Pred. No. 1.8e-149;
Matches 388; Conservative 3; Mismatches 3;
                                                                                                  361 PPEVKFNKPPVFLMIEQNTKSPLFMGKVVNPTGK 394
162 PPEVKFNKPFVFLMIEQNTKSPLFMGKVVNPTQK 395
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Best Local Similarity
                                                                                                                                                                                    RESULT 14
US-11-077-276-14
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        PROTEASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                  Length 522;
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TITLE OF INVENTION: LOW DOSE INHALATION OF FILE REPERENCE; 3942-0020; CURRENT APPLICATION NUMBER: US/11/077,276; CURRENT FILING DATE: 2005-03-09; PRIOR APPLICATION NUMBER: U.S. 60/551,856; PRIOR PILING DATE: 2004-03-09; NUMBER OF SEQ ID NOS: 33 .: SEQ ID NO 20; IEROGIH: 522
        LOW DOSE INHALATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: June 20, 2005, 19:56:55 Job time : 67 secs
                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-11-077-276-20
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June 20, 2005, 16:01:11; Search time 23 Seconds (without alignments) 16.733 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. - protein search, using sw model OM protein Run on:

US-09-885-914B-2 21 Title: Perfect score:

1 RIPR 4 Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters: seq length: 0 seq length: 4 Minimum DB Maximum DB

86

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

neuropeptide Antho FMRPamide - polych cardioexcitatory n 22K superhelical D hypothetical prote glucan 1,4-alpha-g synaptosomal-assoc globulin IV alpha Ig heavy chain CRD T-cell receptor be	receptor b receptor b 2-monoxy rface adhe ttical prot rron 16 d-chain-am nol dehydr nin-potent nin-potent	growth-modulating burshn - chicken thyroglobulin - do gamma subunit of P myosin-light-chain T-cell receptor be protein-glutamine carbon-monoxide de neuropeptide Antho T-cell receptor be T-cell receptor be gene p20% protein T-cell receptor be gene p20% protein T-cell receptor be gene p20% protein T-cell receptor be	១១៥កក្សាទីជម្រើស	process of the control of the contro
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ALIGNMENTS

RESULT 1

phagocytosis-stimulating peptide (tuftsin) - human c;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Dacte: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: A02147
R;Nishioka, K.; Constantopoulos, A.; Satoh, P.S.; Najjar, V.A.
B;Ochem. Biophys. Res. Commun. 47, 172-179, 1972
A;Fille: The characteristics, isolation and synthesis of the phagocytosis stimulating per A;Reference number: A02147; MUID:72187087; PMID:4112769

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thyroliberin - Bombina orientalis
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A; Molecule type: protein
A; Residues: 1-4 < NIS>
A; Residues: 1-4 < NIS>
A; Cross-recences: UNIPROT: P01858
A; Cross-recences: UNIPROT: P01858
A; Note: a peptide having the same structure, physical properties, and biological activit R; Fidalgo, B.V.; Najjar, V.A.
Biochemistry 6, 3186-31392, 1967
A; Reference number: A37502; MUID: 68091045; PMID: 4169272
A; Contents: annotation; immunoglobulin class
C; Comment: An 1967 (called leucockinin) binds reversibly to the cell membrane of neutrophin is essential for maximum stimulation of the phagocytic activity of neutrophils.
C; Superfamily: immunoglobulin C region; immunoglobulin homology
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C;Species: Mus musculus (house mouse)
C;Species: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
C;Accession: 178890
R;Chow, L.M.; Davidson, D.; Fournel, M.; Gosselin, P.; Lemieux, S.; Lyu, M.S.; Kozak, C. Oncogene 9, 3437-3448, 1994
A;Title: Two distinct protein isoforms are encoded by ntk, a csk-related tyrosine protein A;Reference number: 158407; MUID:95060800; PMID:7970703
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Cipecies: Mus musculus (house mouse)
Cipecies: Mus musculus (house mouse)
Cipecies: 184357 # Equiporuk, T.; Pulst, S.
Hum. Mol. Genet. 3, 1075-1079, 1994
A; Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are (A; Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are (A; A; Accession: 154357; MulD:95072570; PMID:7981675
A; Accession: 154357
A; MulD:95072570; PMID:9981675
A; Accession: 154357
A; MulD:95072570; PMID:95072570; PMID:980735
A; Residues: 1-4 <RES>
A; Residues: 1-4 <RES>
A; Residues: 1-4 <RES>
A; Commander Cipecies: GB:L28838; NID:9454836; PIDN:AAA57150.1; PID:9601923
C; Genetics: A; Genetics
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A;Molecule type: DNA
A;Residues: 1-3 «RES»
A;Cross-references: GB:L33339; NID:g609536; PIDN:AAA64432.1; PID:g609538
C;Genetics:
A;Gene: p52ntk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 57.1%; Score 12; DB 2; Length 4; Best Local Similarity 100.0%; Pred. No. 2.8e+05; Matches 2; Conservative 0; Mismatches 0; Indels
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C;Accession: A93750; A01415
R;Desiderio Jr., D.M.; Burgus, R.; Dunn, T.F.; Vale, W.; Guillemin, R.; Ward, D.N.
Org. Mass Spectrom. 5, 221-228, 1971
A;Title: The elucidation of the primary structure of the hypothalamic thyroid stimulating A;Reference number: A93750
                                                                                                                                                                                                                                                                                                                                A,Accession: A93750
A,Modeleule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Rolecule type: protein
A,Residues: 1-3 <-DES>
A;Cross-references: UNIPROT:P01151
R,Burgus, R.; Dunn, T.F.; Desiderio, D.; Ward, D.N.; Vale, W.; Guillemin, R.
Nature 226, 321-325, 1970
A,Title: Characterization of ovine hypothalamic hypophysiotropic TSH-releasing factor.
A,Reference number: A93161; MUD:70163386; PMID:4985794
A,Contents: annotation
A,Rote: physicochemical characteristics and biological activities of the natural and synt C,Superfamily: thyroliberin
C,Reywords: amidated carboxylic acid (Gln) #status experimental
F;1,Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thyroliberin - eastern newt (tentative sequence)
C;Species: Notophthalmus viridescens, Triturus viridescens (eastern newt)
C;Species: Notophthalmus viridescens, Triturus viridescens (castern newt)
C;Accession: A92971; A01415
R;Grimm-Jorgensen, Y.; McKelvy, J.F.
J. Neurochem. 23, 4714-478, 1974
A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain A;Title: Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain A;Reference number: A92971; MUID:75035605; PMID:4214528
A;Reference number: MOID:75035605; PMID:4214528
A;Reference: MOID:75035605; PMID:4214528
A;Residues: 1-3 <GRI>
A;Molecule type: protein
A;Residues: 1-3 <GRI>
A;Note: a peptide with the chromatographic and electrophoretic characteristics of thyrolisting, or glutamic acid
C;Superfamily: thyroliberin
C;Superfamily: thyroliberin
C;Superfamily: amidated carboxylic acid (Gln) #status experimental
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
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C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 09-Jul-2004
C;Accession: A90919; A01415
R;Yasuhara, T.; Nakajima, T.
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Cjaccession: A33802
R;Cockle, S.M.; Aitken, A.; Beg, F.; Smyth, D.G.
Biol. Chem. 264, 7788-7791, 1989
A;Title: A novel peptide, pyroglutemylglutamylproline amide, in the rabbit prostate comp. A;Reference number: A33802; MUID:89255196; PMID:2498305
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R;Koeck, M.; Loeffler, A.; Abel, S.; Glund, K. Plant Mol. Biol. 27, 477-485, 1995 A;Title: CDNA structure and regulatory properties of a family of starvation-induced ribor A;Reference number: $53506; MUID:95201242; PMID:7894013
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A;Title: A molluscan neuropeptide related to the crustacean hormone, RPCH.
A;Reference number: A34626; MUID:90179762; PMID:2310394
                                                                                                                                                                                                                                              thyrotropin-releasing hormone-like peptide - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
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C;Species: Fusinus ferrugineus (ferruginous spindle)
C;Date: 06-Jul.1990 #sequence_revision 06-Jul-1990 #text_change 31-Dec-1993
C;Accession: A34626
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A;Reywords: amidated carboxyl end; pyroglutamic acid
A;Reywords anidated carboxyl end; Gln) #status experimental
F;1/Modified site: pyrrolidone carboxyl end (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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A;Molecule type: protein
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A;Molecule type: protein
A;Residues: 1-4 <KOE>
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Best Local Similarity
Matches 1; Conserv
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A43391
TRH-like tripeptide - alfalfa
Cispecies: Medicago sativa (alfalfa)
Cispecies: Medicago sativa (alfalfa)
Cipate: 15-Uun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Jun-2001
CiAccession: A43391
Rilackey, D.B.
J. Biol. Chem. 267, 17508-17511, 1992
A;Title: Isolation and structural determination of a novel TRH-like tripeptide, pyroGlu-A;Reference number: A43391; MUID:92388092; PMID:1517203
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A; Residues: 1-3 <NAI>
R; Boler, J; Bramann, F; Folkers, K.; Bowers, C.Y.; Schally, A.V.
Biochem. Biophys. Res. Commun. 37, 705-710, 1969
A; Title: The identity of chemical and hormonal properties of the thyrotropin releasing
A; Reference number: A90167; MUID:70039904; PMID:4982117
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Chem. Pharm. Bull. 23, 3301-3303, 1975

A;Title: Occurrence of Pyr-His-Pro-NH-2 in the frog skin.
A;Reference number: A90919; MUID:76138399; PMID:815011
A;Accession: A90319
A;Molecule type: protein
A;Residues: 1-3 4Y8.2
A;Coss-references: UMIPROT:P01151
C;Superfamily: thyroliberin
C;Superfamily: thyroliberin
C;Keywords: amidated carboxyl end; cutaneous gland; hormone; pyroglutamic acid F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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A; Note: biological activities and Rf values (in 17 chromatographic systems)
C; Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
F; 1/Modified site: pyrrolidone carboxylic acid (01n) #status experimental
F; 3/Modified site: amidated carboxyl end (Pro) #status experimental
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C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C;Date: 15-Jun-2001 #sequence_revision 15-Jun-2001 #text_change 15-Mar-2004
C;Accession: A01415
R;Nair, R.M.G.; Barrett, J.F.; Bowers, C.Y.; Schally, A.V.
Biochemistry 9, 1103-1106, 1970
A;Title: Structure of porcine thyrotropin releasing hormone.
A;Reference number: A90560; MUID:70136150; PMID:4984938
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A;Residues: 1-3 <LAC>
C;Keywords: amidated carboxyl end; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;3/Modified site: amidated carboxyl end (Pro) #status experimental
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Microbiol. 152, 335-341, 1989 Arch. Microbiol. Microbiol. 152, 335-341, 1989 Arch. Microbiol. Microbiol. 152, 335-341, 1989 Arch. Microbiol. Microbiol. Microbiol. 152, 335-341, 1989 Arch. Microbiol. Microbiol. Microbiol. Microbiol. 152, 335-341, 1989 Arch. Microbiol. Microbiol. Microbiol. Microbiol. 152, 335-341, 1989 Arch. Microbiol. M
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metallothionein-A - rainbow trout (fragment)
c;Species: Oncorhynchus mykiss (rainbow trout)
c;Species: Oncorhynchus mykiss (rainbow trout)
c;Species: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
c;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
c;Caccession: E1049
R;Olsson, P.E.; Kiling, P.; Erkell, L.J.; Kille, P.
Eur. J. Biochem. 230, 344-349, 1995
A;Title: Structural and functional analysis of the rainbow trout (Oncorhyncus mykiss) and A;Reference number: I51049; MUID:95324545; PMID:7601121
A;Accession: I51049
A;Access
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ribosomal protein YmL1, mitochondrial, questionable - yeast (Saccharomyces cerevisiae) (1
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C; Date: 23-Apr-1993 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
C; Cicoment Discreption 15-Sep-1991
A; Title: Extended N-terminal sequencing of proteins of the large ribosomal subunit from Na; Reference number: S17255
A; MulD:91285106; PMID:2060626
A; Molecule type: protein
A; Residues: 1-4 <RRO>
A; Residues: 1-4 <RRO>
A; Cross_references: UNIPROT:P36515
C; Comment: A coding region for this protein could not be identified in the genome of Sacc C; Genetics:
C;Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, met C;Keywords: oxidoreductase
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C;Keywords: mitochondrion; protein biosynthesis; ribosome
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4 AA

Perfect score:

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Minimum DB Maximum DB

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MEDLINGE-680910415; PubMed-4169272;
MEDLINGE-68091045; PubMed-4169272;
Fidalgo B.V., Najjar V.A.;
"The physiological role of the lymphoid system. VI. The stimulatory effect of leucophilic gamma globulin (leucokinin) on the phagocytic activity of human polymorphonuclear leucocyte.";
Biochemistry 6:3386-3392(1967).
-- MISCRELLAMSTOUS: An IgG (called leucokinin) binds reversibly to the cell membrane of neutrophils in the blood. Leucokininase on the membrane releases the active peptide tuftsin from the gamma chain. Tuftsin is essential for maximum stimulation of the phagocytic activity of neutrophils.

MIN; 19150: --
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MEDLINE=92270459; PubMed=1821096; DOI=10.1016/0196-9781(91)90190-Z;
Nothacker H.-P., Rinehart K.L. Jr., McFarlane I.D.,
Grimmelikhuijzen C.J.P.;
                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=72187087; PubMed=4112769; Nishloka K., Constantopoulos A., Satoh P.S., Najjar V.A.; Nishloka K., Constantopoulos A., Satoh P.S., Najjar V.A.; The characteristics, isolation and synthesis of the phagocytosis stimulating peptide tuftsin."; Biochem. Biophys. Res. Commun. 47:172-179(1972).
                                                                                                                                                                                                                                 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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GO; GO:0006809; P:phagocytosis; NAS.
Direct protein sequencing.
SEQUENCE 4 AA; 501 MW; 74176321C000000 CRC64;
                                                                                                                                                Phagocytosis-stimulating peptide (Tuftsin).
Homo sapiens (Human).
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28-FEB-2003 (Rel. 41, Last sequence update)
26-UTL-2004 (Rel. 44, Last annotation update)
Antho-Rlamide I (Contains: Antho-Rlamide II).
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                                                                                                                                                               June 20, 2005, 15:59:16; Search time 109.5 Seconds (without alignments) 18.706 Million cell updates/sec
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016047
PAR3_HIRME
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ILME_SEPOF
EOSI_HUMAN
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GRWM HUMAN
DCMS PSECH
FFKA ANTEL
Q96ATO
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                                                                                                                        OM protein - protein search, using sw model
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1: uniprot_sprot:*
2: uniprot_trembl:*
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THYL PIG
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"Occurrence of Pyr-His-Pro-NH2 in the frog skin.";
Chem. Pharm. Bull. 23:3301-3303(1975)
-1- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/neuromodulator in the central and peripheral nervous systems (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THYL BOMOR STANDARD; PRT; 3 AA.
P62976; POLIB;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last sequence update)
25-GCT-2004 (Rel. 45, Last annotation update)
Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (FORI-Leleasing factor) (Profixelin).
Bombina oriehtalis (Oriental fire-bellied toad).
Butazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
MCBI_TaxID-8936;
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expansion behaviour of sea anemones may be coordinated by two
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Amidation, Direct protein sequencing, Pyrrolidone carboxylic acid.
                                                               muscle
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P62971, P01151;
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
25-OGT-2004 (Rel. 45, Last annotation update)
Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH releasing factor)
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                 inhibitory neuropeptides, Antho-KAamide and Antho-RIamide.";
Proc. R. Soc. Lond., B, Biol. Sci. 253:183-188(1993).
-!- FUNCTION: Inhibits spontaneous contractions in several mugroups. May be involved in the expansion phase of feeding
                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                  DB 1; Length 4;
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                                                                                                                          -1- SUBCELLUIAR LOCATION: Secreted.
-1- TISSUE SPECIFICITY: Neuron specific.
Amidation; Direct protein sequencing; Neuropeptide CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 3 3 Proline amide.
3.AA, 380 MW; 7761F6B00000000 CRC64;
                                                                                                                                                                                                                                                                      4 AA; 598 MW; 60441B59A000000 CRC64;
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o. 1.6e+06;
                                                                                                                                                                                                         Antho-RIamide II.
3-phenyllactic acid.
Isoleucine amide.
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0; Mismatches
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100.0%; Pred. No. 1.6
tive 0; Mismatches
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SUBCELLULAR LOCATION: Secreted.
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                                                                                                      behaviour in sea anemones.
                                                                                                                                                                                                                                                                                                                  42.9%;
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ID THYL NOTVI
AC P62971,
DT 21-JUL
DT 25-JUL
DE Thyroli
DE releasi
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EFFE COCCORTEFF S
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Grimm-Joergensen Y., McKelvy J.F.;
"Biosynthesis of thyrotropin releasing factor by newt (Triturus viridescens) brain in vitro. Isolation and characterization of thyrotropin releasing factor.";
J. Neurochem. 23:471-478(1974).
-!- FUNCTION: TRH functions as a regulator of the biosynthesis of TSH in the anterior pituitary gland and as a neurotransmitter/
neuromodulator in the central and peripheral nervous systems.
-!- SUBCELLULAR LOCATION: Secreted.
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MOD_RES
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia; Batrachia, Caudata; Salamandroidea, Salamandridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THYL PIG STANDARD; PRT; 3 AA. P65958; P01151.
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
25-GCT-2004 (Rel. 45, Last amnotation update)
Thyroliberin (Thyrotropin releasing hormone) (TRH) (Thyrotropin releasing factor) (TSH-releasing factor).
Notophthalmus viridescens (Eastern newt) (Triturus viridescens)
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5. 1.6e+06;
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Nair R.M.G., Barrett U.T., Bowers C.Y., Schally A.V.;
"Structure of porcine thyrotropin releasing hormone.";
Biochemistry 9:1103-1106(1970).
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3 AA; 380 MW; 7761F6B00000000 CRC64;
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3 AA; 380 MW; 7761F6B00000000 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.3%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                  MEDLINE=75035605; PubMed=4214528;
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Best Local Similarity
Matches 1; Conserv
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                                                                                                   NCBI_TaxID=8316;
                                                                            Notophthalmus
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FEBS Lett. 284:51-56(1991).
-!- FUNCTION: Putative component of the large subunit of mitochondrial
                                                  MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V; Grohmann L., Graack H.-R., Kruft V., Choli T., Goldschmidt-Reisin S.
                   Kraut M., Hugendieck I., Herwig S., Meyer O.;
"Homology and distribution of CO dehydrogenase structural genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Extended N-terminal sequencing of proteins of the large ribosomal subunit from yeast mitochondria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Pungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; 817255; 817255.
Direct protein sequencing; Mitochondrion; Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Mitochondrial 60S ribosomal protein L1 (YmL1) (Fragment)
                                                                                                                                                                                                                                                                                                          h 33.3%; Score 7; DB 1; Length 4; Similarity 100.0%; Pred. No. 1.6e+06; 1; Conservative 0; Mismatches 0; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               h 33.3%; Score 7; DB 1; Length 4; Similarity 100.0%; Pred. No. 1.6e+06; 1; Conservative 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                      Direct protein sequencing; Molybdenum; Oxidoreductase.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Interleukin 2 receptor alpha-subunit (Fragment)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                             4 AA; 441 MW; 7761E876F000000 CRC64;
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MEDLINE=90055678; PubMed=2818128;
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Best Local Similarity
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SEQUENCE
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P36515;
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YLM1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ward D.N.;
"The elucidation of the primary structure of the hypothalamic thyroid stimulating hormone releasing factor of ovine origin by means of mass spectrometry.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factor.";
Nature 226:321-325 (1970).

-1- FUNCTION: TRH functions as a regulator of the biosynthesis of
in the anterior pituitary gland and as a neurotransmitter/
in the anterior pituitary gland and peripheral nervous systems.

-1- SUBCELLULAR LOCATION: Secreted.

PIR; A93750; RHSHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amidation; Direct protein sequencing; Pyrrolidone carboxylic acid. MOD RES 1 Pyrrolidone carboxylic acid. MOD RES 3 Proline amide. SEQUENCE 3 AA, 380 MW, 7761F6B000000000 CRC64;
                                                                                                                                                                                                                                                                                  Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Caprinae, Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUB-Hypothalamus;
Desiderio D.M. Jr., Burgus R., Dunn T.F., Vale W., Guillemin R.,
                                                                                                                        THYL SHEEP

AC P62969; PO1151;

AC 121-JUL-1986 (Rel. 01, Last sequence update)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DT 25-OCT-2010 (Rel. 45, Last annotation update)

DT 25-OCT-2010 (Rel. 45, Last annotation update)
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=70163386; PubMed=4985794; Burgus R., Dunn T.F., Desiderio D.M., Ward D.N., Vale W., Guillemin R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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01-FEB-1991 (Rel. 17, Last sequence update)
05-JUJ-2004 (Rel. 44, Last annotation update)
Carbon monoxide dehydrogenase large chain (EC 1.2.99.2)
dehydrogenase subunit L) (CO-DH L) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 3;
                                                                                                                                                                                                                                                   releasing factor) (TSH-releasing factor) (Protirelin)
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Matches 1; Conserv
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NCBI_TaxID=290;
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SPECIES-H.trivolvis; TISSUE-Kidney; MEDLINE-94486417; Pubmed-7912428; DOI=10.1016/0196-9781(94)90166-X; Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.; "FMRRamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
Evans B.D., Pohl U., Kartsonis M.A., Calabrese R.L.;
"Identification of RFamide neuropeptides in the medicinal leech.";
Peptides 12:897-908(1991).
                                                                                                                MEDITNE-92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N; Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; "Identification of RFamide neuropeptides in the medicinal leech."; Peptides 12:897-908(1991).
-: SUBCELULAR LOCATION: Secreted.
-: SIMPLARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hirudo medicinalis (Medicinal leech), and
Helisoma trivolvis (Snail).
Bukaryota; Merazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
Hirudo medicinalis (Medicinal leech).
Bukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NCBI_TaxID=6421;
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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1; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                Query Match 23.8%; Score 5; DB 1; Length 4; Best Local Similarity 100.0%; Pred. No. 1.6e+06; Matches 1; Conservative 0; Mismatches 0; Indel&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amidarion; Direct protein sequencing; Neuropeptide.
MOD RES 4 4 Phenylalanine amide.
SEQUENCE 4 AA; 582 MW; 69D40729A000000 CRC64;
                                                                                                                                                                                                                                                               Amidation; Direct protein sequencing; Neuropeptide.

MOD RES

4 4 4 Phenylalanine amide.

SEQUENCE 4 AA; 616 MW; 69D4068B30000000 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
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Best Local Similarity
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ID FLRN_ANTEL
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FLRF_HIRME
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Matches
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                                                                            SEQUENCE FROM N.A.

MEDLINE=92062171; PubMed=1840490;
Mercken L., moras V., Hemon L., Lionne B., Bousseau A.,
Mercken L., woras V., Hemon L., Lionne B., Bousseau A.,
Dautry-Varsat A., Collins M., Mayaux J.F.;
"An exon 5-deleted mRNA encodes a functional interleukin 2 receptor alpha-subunit.";
Biochem. Biophys. Res. Commun. 180:1390-1395(1991).
Biochem. Biophys. Res. Commun. 180:1390-1395(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N; Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; "Identification of RFamide neuropeptides in the medicinal leech."; Peptides 12:897-908(1991).
-1- SUBCELLULAR LOCATION: Secreted.
-1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
                                                                                                                                                                                                                                                           GO; GO:0005525; F:GTP binding; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
InterPro; IPR001806; Ras trnsfrmng.
PRINTS; PR00449; RASTRNSFRNNG.
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
05-NUL-2004 (Rel. 44, Last annotation update)
FWRFamide-like neuropeptide YLRF-amide.
Hirudo medicinalis (Medicinal leech).
Eukaryota: Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudinea;
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MOD RES
4 4 4 Phenylalanine amide.

SEQUENCE 4 AA; 598 MW; 69D4073B30000000 CRC64;
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01-NOV-1995 (Rel. 32, Last sequence update)
02-UU-2004 (Rel. 44, Last annotation update)
PWRFamide-like neuropeptide YMRF-amide.
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100.0%; Pred. No. 1.6
tive 0; Mismatches
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Best Local Similarity
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                               NCBI_TaxID=9606;
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FAR4 HIRME
ID FAR4 HIRME
AC P42563;
DT 01-NOV-1995
DT 01-NOV-1995
DT 05-JUL-2004
DE FMRFamide-li
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SEQUENCE
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LUXE VIBFI
ID LUXE VIBFI
AC P24272;
                                                                                                                                                                                                                                                                            trivolvis."
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"Purification and characterization of a cardioexcitatory neuropeptide from the central ganglia of a bivalve mollusc.";
Prep. Biochem. 7:261-281(1977).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
-- SUBCELLULUAR LOCATION: Secreted.
-- TISSUB SPECIFICITY: Neuron specific.
--- MASS SPECTROMETRY: MW=549.3; METHOD=FAB; RANGE=1-4; NOTE=Ref.1.
PIR; A35779; A35779.
Modelion; Direct. protein sequencing; Neuropeptide.
MOD_RES
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MEDLINE=90259866; PubMed=2342992; DOI=10.1016/0196-9781(90)90113-J;
                                                                                                                                                                                                      SEQUENCE, AND MASS SPECTROMETRY.

MEDLINE=90319122; PubMed=1973541;

Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,

Reinscheid R.K., Nothacker H.-P., Staley A.L.;

"Isolation of L.3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sanemone neuropeptide containing an unusual amino-terminal blocking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krajniak K.G., Price D.A.; "Authentic FMRFamide is present in the polychaete Nereis virens."; Peptides 11:75-77(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Mollusca; Bivalvia; Heteroconchia; Veneroida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE, AND SYNTHESIS.
SPECIES-M.nimbosa; TISSUE-Cerebral pedal, and Visceral ganglion;
MEDLINE-77215956; PubMed-877582;
Price D.A., Greenberg M.J.;
"Structure of a molluscan cardioexcitatory neuropeptide.";
Science 197:670-671(1977).
                                                                                                  Anthopleura elegantissima (Sea anemone).
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
Nynantheae; Actiniidae; Anthopleura.
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4 AA; 549 MW; 64540729A0000000 CRC64;
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POS-JUL-2004 (Rel. 44, Last annotation update)
POS-JUL-2004 (Rel. 44, Last annotation update)
POSTREmide (Peak C) (Cardioexcitatory neuropeptide)
Macrocallista nimbosa (Sun-ray clam),
Macrocallista nimbosa (Sun-ray clam),
Hirudo medicinalis (Medicinal leech), and
Helisoma trivolvis (Snail).
             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Pred. No. 1.0 ive 0; Mismatches
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NCBI_TaxID=6594, 6353, 6421, 27815;
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MEDLINE-78012038; PubMed-909875;
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les 1; Conserv
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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J. Bacteriol. 172:6797-6802(1990).
-I- FUNCTION: Acyl-protein synthetase activates tetradecanoic acid. It is a component of the fatty acid reductase complex responsible for converting tetradecanoic acid to the aldehyde which serves as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1992 (Rel. 21, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Long-chain-fatty-acid--luciferin-component ligase (BC 6.2.1.19) (Acyl-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptides 15:31-36(1994).

-!- FUNCTION: Myoactive; cardioexcitatory substance. Pharmacological activities include augmentation, induction, and regularization of cardiac contraction.

-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
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"A new Vibrio fischeri lux gene precedes a bidirectional termination
                                                                                                                                                                                                                                                                                   SPECIES=H.trivolvis, TISSUB=Kidney;
MEDLINE=9436411; PubMed=7912428; DOI=10.1016/0196-9781(94)90166-X;
Madrid K.P., Price D.A., Greenberg M.J., Khan H.R., Saleuddin A.S.M.
"FMRPamide-related peptides from the kidney of the snail, Helisoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       substrate in the luciferase-catalyzed reaction. CATALYIIC ACTIVITY: ATP + an acid + protein = AMP + diphosphate
SPECIES=H.medicinalis; MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N; Evana B.D., Pohl J., Kartsonis M.A., Calabrese R.L.; Identification of RPamide neuropeptides in the medicinal leech."; Peptides 12:897-908(1991).
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PIR; A60418; A60418.
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Ligase; Luminescence.

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SQ SEQUENCE 3 AA; 374 MW; 6AA330300000000 CRC64;

Query Match

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps

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Search completed: June 20, 2005, 16:33:43 Job time: 111.5 secs

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                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence is that of alpha 1 antitrypsin Portland (AAT Portland) residues 355-358 which is a furin endopeptidase inhibitor. The AAT variant can be used to inhibit bacterial infections, esp. those caused by Corynebacterium dipthteriae, Bacillus anthracis and Pseudomonas aeruginosa, and to treat viral infections, esp. HIV and influenza. (Updated on 25-MAR-2003 to correct PN field.)
   Φ
Adr49058 Caspase Aar30753 IgE-mast
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                                                                                                                                                                                                                                                                                                                       endopeptidase inhibitor; variant; bacterial infection;
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ADR49058
AAR30753
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                                                                                                                                                             AAR59927 standard; peptide; 4 AA.
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The present sequence is the reactive site loop of alpha-1 antitrypsin mutated variant Portland (also termed PDX). This portion of the PDX protein acts as the pharmacophore necessary for bological activity. The RSL forms a rigid backbone having positively-charged guanidino residues of each of the Arg residues extending in space away in the same direction from the rest of the PDX protein. Peptides or peptide minetics comprising this sequence inhibit bacterial toxins that are processed at a consensus furin recognition site, when administered in therapeutically effective amounts. Endoproteolytic activation of bacterial toxins and endolytic maturation of viral proteins is blocked by the peptide and peptide mimetics. This is useful in treating infections of cells by bacteria and viruses. It may also be used to inhibit processing of biologically active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New furin endoprotease inhibitor that mimics a specific region of alphalantitrypsin Portland mutant, for treatment and prevention of bacterial and viral infection.
furin recognition site, endoproteolytic activation;
endolytic maturation viral protein; bacterial infection; viral infection.
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                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADJ57388 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 4; 108pp; English.
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Cromlish JA

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(RECL-) INST RECH CLINIQUES MONTREAL.
                                                                                      01-AUG-2001; 2001WO-CA001118.
                                                                                                                  01-AUG-2000; 2000CA-02313828
                                                                                                                                                                            Seidah NG, Chretien M,
                                                                                                                                                                                                      WPI; 2002-280632/32.
                              WO200210354-A2
   Unidentified.
                                                           07-PEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU78526;
                                                                                                                                                                                                                                                                                  enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
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                                                                                                                                                                                                                                                                                                                  The present sequence is that of a peptide fragment of alpha-1-
antitrypsin. Convertase inhibitors of the invention may be derivatives of
antitrypsin. Convertase enzymes act, both extracellularly have
cestablished that convertase enzymes act, both extracellularly and
intracellularly, to cause the activation of latent transforming growth
factor-beta (TGP-beta) in the extracellular space at the site of a wound
of a fibrotic conditions. Thus, the present invention relates to use of
convertase inhibitors for the reduction of scarring during the healing of
convertase inhibitors for the reduction of scarring during the healing of
convertase inhibitors for the reduction of scarring during the healing of
convertase inhibitors for the reduction of scarring during the healing of
convertase inhibitor conditions,
convertase inhibitor conditions
conditions at fibrotic condition is a fibrotic disorder such as
convertase lunds (all claimed). The convertase inhibitor can also be used
conditions the treatment of hypertropic and keloid scars, scarring in the heart,
conditions the pelvis in the region of the
convertase leading to infertility, scarring following injury to the
convertase leading to infertility, scarring following a stroke
convertase infarction, central nervous system fibrosis following a stroke
cor neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
cor neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
cor neurodegenerative disorders (e.g. Alzheimer's disease), proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                 Use of a convertase inhibitor in the manufacture of a medicament for reducing scarring during the healing of wounds or reducing fibrosis in the treatment of fibrotic conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alzheimer's disease; beta amyloid precursor protein; BACB; beta-site APP cleaving enzyme; nootropic; neuroprotective; beta-site amyloid precursor protein (APP) -cleaving enzyme; APP; BACE secretase/sheddase; neurodegenerative disorder; proprotein convertase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95.2%; Score 20; DB 8; Length 4; 75.0%; Pred. No. 1.8e+06; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BACE proprotein convertase cleavage site.
                                                                                                                                                                                                                                                                                             Disclosure; Page 10; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU78507 standard; peptide; 4 AA.
                                                                                   23-JUL-2003; 2003WO-GB003159.
                                                                                                                  24-JUL-2002; 2002GB-00017136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUN-2002 (first entry)
                                                                                                                                                                          Ferguson MWJ, Brunner G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 75.0 hes 3; Conservative
                                                                                                                                                                                                    WPI; 2004-180270/17.
                                                                                                                                             (RENO-) RENOVO LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4 AA; .
                              WO2004009113-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:|.|
RVPR 4
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Unidentified
                                                         29-JAN-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU78507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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This invention relates to a novel method for modulating activity of betasite amyloid precursor protein (APP)-cleaving enzyme (BACE)

Secretasaes/sheddase. Cleavage of BACE by this enzyme results in the generation of a soluble BACE which enhances the production of the actiology of Alzeimer's disease. Inhibition of BACE secretase can be actiology of Alzeimer's disease. Inhibition of BACE secretase can be achieved by administration of an antisense nucleotide molecule capable of hybridising with BACE mRNA, by using a ribozyme that targets and degrades and inhibitor of BACE secretase activation. The methods of the enzyme with BACE or using an antibody or antagonist that can function as an inhibitor of BACE secretase activation. The methods of the creatment of as an inhibitor of BACE secretase activation. The methods of the creatment of a creatment of a natural processes sheddase by preventing cleavage of BACE, which is useful for the treatment of a neurodegenerative disorder characterised by the generation of Abeta protein, especially Alzheimer's disease. The invention also comprises a method for agentation of an agent that can alter the ability of BACE can be used for high throughput screening of candidate molecules. The invention also comprises a method for determining whether an individual is at risk of developing a neurodegenerative disorder characterised by the generation of Abeta protein by measuring the levels of BACE cerminal cleavage products in a sample or tissue where an individual is at risk of developing a person at risk. The present sequence represents the BACE proprotein convertase cleavage site used to create the prosegment deletion mutants of the invention
Modulating activity of beta-site amyloid precursor protein-cleaving enzyme secretase/sheddase for treatment of neurodegenerative disorder characterized by generation of Abeta protein, by preventing cleavage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      beta-site APP cleaving enzyme; nootropic; neuroprotective;
beta-site amyloid precursor protein (APP)-cleaving enzyme; APP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 19; DB 5; Length 4;
Pred. No. 1.8e+06;
1; Mismatches 0; Indels
                                                                                                                                                                                                    Disclosure, Page 19, 64pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU78526 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4 AA;
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This invention relates to a novel method for modulating activity of betasite amyloid precursor protein (APP)-cleaving enzyme (BACE)

Secretases/shedase. Cleavage of BACE by this enzyme results in the generation of a soluble BACE which enhances the production of the awyloidogenic peptide Abeta which has been shown to be involved in the actiology of Alzheimer's disease. Inhibition of BACE secretase can be achieved by administration of an antisense nucleotide molecule capable of Abbidiang with BACE mRNA, by using a ribozyme that targets and degrades con hybridising with BACE mRNA, by using a ribozyme that targets and degrades of the enzyme with BACE or using an antibody or antagonist that can function as an inhibitor of BACE secretase mRNA, mith a peptide that can interfere with binding of the enzyme with BACE or using an antibody or antagonist that can function as an inhibitor of BACE secretase states/sheddase by preventing cleavage of BACE, which is useful for the treatment of a neurodegenerative disorder characterised by the generation of Abeta control of an agent that can alter the ability of BACE secretase to associate with and process a known substrate, this method control of an agent that can alter the ability of BACE secretase to associate with and process a known substrate, this method control also comprises a method for determining whether an individual is at risk of developing a neurodegenerative disorder characterised by the generation of Abeta protein by measuring the levels of BACE of terminal cleavage products in a sample or tissue where an increase in cleavage products in a sample or tissue where an increase in cleavage products in a sample or tissue where an increase in cleavage products in a sample or tissue where an increase in cleavage products in a sample or tissue where an increase in cleavage products in a sample or tissue secretasing
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                                                                                                                                                                                                                                                                                                                                                                                                               Modulating activity of beta-site amyloid precursor protein-cleaving enzyme secretase/sheddase for treatment of neurodegenerative disorder characterized by generation of Abeta protein, by preventing cleavage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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BACE secretase/sheddase; neurodegenerative disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antibacterial peptide from hHBP #133.
                                                                                                                                                                                                                                                                           (RECL-) INST RECH CLINIQUES MONTREAL.
                                                                                                                                                                                                                                                                                                                         Cromlish JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Page 3; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADK42152 standard; peptide; 4 AA.
                                                                                                                                                                                   01-AUG-2001; 2001WO-CA001118
                                                                                                                                                                                                                                01-AUG-2000; 2000CA-02313828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                         Chretien M,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-280632/32.
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|:||
RLPR 4
                                                                                          WO200210354-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4 AA;
                                             Unidentified
                                                                                                                                        07-FEB-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                         Seidah NG,
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The invention relates to an antibacterial peptide conforming to the generic peptide sequence appearing as ADK42632, the motif being derived from analysis of the protein sequences of human heparin binding protein, hHBP, pig pHBP and human neutrophil elastase (hNLB). Also included are a process for producing the new peptide (comprising providing an expression vector containing a DNA sequence encoding one or more of the abovementioned amino acid sequence encoding one or more of the above mentioned amino acid sequences, reansforming host cells with the vector, culturing the transformed host cells and purifying the expressed peptide is capable of inhibiting or stimulating the secretion of cytokine IL-6 from monocytes. The peptides are useful in manufacturing a medicament for the treatment of Gram-negative or Gram-positive bacterial infection, such as sepsis, severe sepsis, septic shock, disseminated intravascular coagulation, meningococcal meningitis or pneumococcal pneumonia. These cast is also be used in manufacturing a medicament for the stimulation or first the stimulation or firs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-turn region, cyclic peptide, antimicrobial; disinfectant, therapy; preservative, amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides of heparin-binding protein and/or human neutrophil elastase for manufacturing a medicament for the treatment of e.g. bacterial infections, disseminated intravascular coagulation, cancer or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibition of inflammatory response, for the prevention of cell apoptosis, or for the treatment of individuals having suppressed immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        system, cancer, autoimmune diseases and/or trauma. The present sequence represents an antibacterial peptide of the invention derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
  meningococcal meningitis;
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disseminated intravascular coagulation; meningococcal meningiti
pneumococcal pneumonia; inflammatory response; cell apoptosis;
suppressed immune system; cancer; autoimmune diseases; trauma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17; DB 8; Length 4; Pred. No. 1.8e+06; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 52; SEQ ID NO 134; 211pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Norris K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW52385 standard; peptide; 4 AA.
                                                                                                                                                                                                                                                                                                                                          15-AUG-2002; 2002DK-00001212.
19-AUG-2002; 2002US-0404155P.
27-JUN-2003; 2003DK-00000987.
                                                                                                                                                                                                                                                                                        14-AUG-2003; 2003WO-DK000542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.0%;
75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Djurup R, Flodgaard HJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LEUK-) LEUKETOCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-257185/24.
                                                                                                                                                                            WO2004016653-A2
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                                                                                                                                                                                                                                   26-FEB-2004
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resistant Streptococcus pneumoniae. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and protozoa. Apart from clinical uses, (1) are also used as disinfectants and preservatives for medical equipment, foods, cosmetics etc., also for treatment of plant diseases. Compared with non-cyclised analogues (i.e. tachyplesin and protegrin type peptides), (1) and are more effective, with better bioavailability and/or serum half-life (increased resistance to proteolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-turn region; cyclic peptide; antimicrobial; disinfectant; therapy; preservative; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                                                                                                                                                             New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear analogues.
                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents a beta-turn region used in a peptide of the invention. The peptides are cyclic peptides (1), which have: (a) an amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological ph; and (c) at least one basic amino acid (aa) in LR or TR. (1) are broad spectrum antimicrobials, specifically for use against E. coli, bedudomonas aeruginosa, methicillin-resistant Staphylococcus aureus (MRSA), vandomycin-resistant Enterococcus faecium and penicillin-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Beta-turn region used in cyclic peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.2%; Score 16; DB 2; Length 4; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                   Claim 3; Page 149; 160pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW52384 standard; peptide; 4 AA.
                                                                                                                                                                                        (INTR-) INTRABIOTICS PHARM INC
                                                                                                                     97WO-US012974.
                                                                                                                                                       96US-00685589.
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                                                                                                                                                                                                                            Chen J;
                                                                                                                                                                                                                                                            WPI; 1998-120472/11.
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                                                  WO9803192-AL.
                                                                                                                                                       24-JUL-1996;
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                                                                                    29-JAN-1998
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                  Synthetic.
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                                                                                                                                                                                                                            Chang C,
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Gaps ö

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This sequence represents a beta-turn region used in a peptide of the invention. The peptides are cyclic peptides (I), which have: (a) an amplipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological ph; and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad specifically for use against E. coli, peeudomonas aeruginosa, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faecium and penicillin-resistant Streptococcus penemoniae. More generally they are active against Gram-positive or -negative bacteria, fungi, yeast and protozoa. Apart from clinical uses, (I) are also used as disinfectants and protozoare treatment of plant diseases. Compared with non-cyclised analogues (i.e. treatment of plant diseases. Compared with non-cyclised analogues (i.e. tachyplesin and protegrin type peptides), (I) and are more effective, with better bloavailability and/or serum half-life (increased resistante to protecolysis). They are more suitable for oral administration, can be used at lower doses and are unlikely to induce development of resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Beta-turn region, cyclic peptide; antimicrobial; disinfectant; therapy; preservative; amphipathic anti-parallel beta-sheet region; plant disease.
                                                                                                                                                       New cyclic peptide(e) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear analogues.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.2%; Score 16; DB 2; Length 4; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indel8
                                                                                                                                                                                                                               Claim 3; Page 148; 160pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW52383 standard; peptide; 4 AA.
                                                 (INTR-) INTRABIOTICS PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Conservative
                                                                                    Gu L, Chen J;
                                                                                                                      WPI; 1998-120472/11.
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Best Local Similarity
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                24-JUL-1996;
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                                                                                    Chang C,
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(LR) and

Gu L, Chen J;

Chang C,

WPI; 1998-120472/11.

This sequence represents a beta-turn region used in a peptide of the invention. The peptides are cyclic peptides (I), which have: (a) an amphipathic anti-parallel beta-sheet region (SR), a loop region (LR) and a beta-turn region (TR); (b) a net positive charge at physiological pH; and (c) at least one basic amino acid (aa) in LR or TR. (I) are broad specifically for use against B. coli, peeudomonas aeruqinosa, methicillin-resistant Staphylococcus aureus (MRSA), vancomycin-resistant Enterococcus faccium and penicillin-resistant Streptococcus penemoniae. More generally they are active against Gram-positive or -negative bacteria, fungl, yeast and protozoa. Apart from clinical uses, (I) are also used as disinfectants and protozoa. Treatment of plant diseases. Compared with non-cyclised analogues (i.e. treatment of plant diseases. Compared with non-cyclised analogues (i.e. treatment of plant diseases. Compared with non-cyclised analogues (i.e. trachyplesin and protegrin type peptides), (I) and are more effective, with better bioavailability and/or serum half-life (increased resistance to protecolysis). They are more suitable for oral administration, can be unlikely to induce development of resistant New cyclic peptide(s) with antimicrobial activity - contain amphipathic beta-sheet, loop and beta-turn regions, have better activity, bio:availability and protease resistance than linear analogues. Gaps Reactive site loop, RSL, alpha-1 antitrypsin variant Portland; PDX, Portland protein, pharmacophore; guanidino residue, peptide mimetic; bacterial toxin; furin recognition site; endoproteolytic activation; endolytic maturation; viral protein; bacterial infection; Generic sequence-2 of the reactive site loop of Portland protein. ö 76.2%; Score 16; DB 2; Length 4; 100.0%; Pred. No. 1.8e+06; rive 0; Mismatches 0; Indels /note= "Any amino acid residue" Location/Qualifiers Claim 3; Page 148; 160pp; English. AAY44204 standard; protein; 4 AA. (UYOR-) UNIV OREGON HEALTH SCI 99WO-US007776 (first entry) 3; Conservative WPI; 1999-620190/53 Query Match Best Local Similarity Thomas G; Misc-difference viral infection RIP 3 RIP 3 Sequence 4 AA; Homo sapiens. 25-JAN-2000 08-APR-1999; 08-APR-1998; WO9951624-A1 14-OCT-1999 Synthetic AAY44204; Jean F, Matches 유

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The present sequence is the reactive site loop of alpha-1 antitrypsin mutated variant Portland (also termed PDX). This portion of the PDX protein acts as the pharmacophore necessary for biological activity. The RSL forms a rigid backbone having positively-charged quantidno residues of each of the Arg residues extending in space away in the same direction from the rest of the PDX protein. Peptides or peptide mimetics comprising this sequence inhibit bacterial toxins that are processed at a consensus furin recognition site, when administered in therapeutically effective manuals. Endoproteolytic activation of bacterial toxins and endolytic maturation of viral proteins is blocked by the peptide and peptide mimetics. This is useful in treating infections of cells by bacteria and viruses. It may also be used to inhibit processing of biologically active
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             New furin endoprotease inhibitor that mimics a specific region of alphal-
antitrypsin Portland mutant, for treatment and prevention of bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes cyclic peptides (1): (i) comprising an amphiphild canti-parallel beta-sheet region (A), a loop region (B) and a beta-turn (C); (ii) having net positivy charge at physiological pH; and (iii) including at least one basic amino acid (aa) in (B) or (C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biocidal; bacteria; yeast; Candida species; fungi; protozoa; psocharia coli; Pseudomonas aeruginosa; infection; preservative; vancomycin-resistant Enterococcus faecium; disinfectant; food; methicillin-resistant Staphylococcus aureus; medical equipment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; antimicrobial; amphiphilic beta-sheet; biostatic;
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Pred. No. 1.8e+06;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY09581 standard; peptide; 4 AA
                                                                                         Claim 1; Page 8; 108pp; English
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75.0%;
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                                    antitrypsin Portland
and viral infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RXPR 4
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4 AA;
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                                                                                                                                                                                                                                                                                                                                                           proteins
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Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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claimed cyclic peptides and pay17301 to AAY17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-spectrum artimicrobials (bioseratic or biocidal), effective against bacteria, yeast (e.g. Candida species), fungi and protozoa. Particularly they are used to control Bscherichia coli, Pseudomonas aeruginosa, vancomycin-resistant Enterococus acuseus and penicillin-resistant Staphylococcus aureus and penicillin-resistant Staphylococcus aureus and penicillin-resistant Staphylococcus and casinfections, in animals or plants, also as preservatives and disinfections, for medical quipment, foods, cosmetics, optionally as mixtures or in combination with other antimicrobials. Compared with linear analogues, (I) are more effective with better bioavailability and/or serum half-life (better resistance to proteolysis, allowing lower doses and making them more suitable for oral delivery). Since (I) are strunturally related to naturally occurring antimicrobial peptides, they are less likely to induce development of resistant strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4 AA;
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Gaps ö 0; Indels 76.2%; Score 16; DB 2; Length 4; 100.0%; Pred. No. 1.8e+06; ive 0; Mismatches 0; Indels 3; Conservative Best Local Similarity 1 RIP 3 Query Match Matches ò

RIP 3

AAY09582 standard; peptide; 4 AA.

AAY09582;

(first entry)

21-JUL-1999

Antimicrobial cyclic peptide beta-turn region SEQ ID NO:29.

blocidal; bacteria; yeast; Candida species; fungi; protozoa; Bacherichia coli; Pseudomonas aeruginosa; infection; preservative; vancomyclin-resistant Entercoccus faecium; disinfectant; food; methicillin-resistant Staphylococcus aureus; medical equipment; penicillin-resistant Streptococcus pneumoniae; cosmetic. Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic;

Synthetic

WO9921879-A1.

06-MAY-1999

97WO-US019557. 27-OCT-1997; (INTR-) INTRABIOTICS PHARM INC

Gu L, Chen J; Chang C,

Antimicrobial cyclic peptides with amphiphilic beta-sheet region WPI; 1999-312941/26.

The present invention describes cyclic peptides (I): (i) comprising an amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a beta-turn (C); (ii) having net positive charge at physiological pH; and (iii) including at least one basic amino acid (aa) in (B) or (C). AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically claimed cyclic peptides and peptide segments. (I) are broad-spectrum antimicrobials (biostatic or biocidal), effective against bacteria, yeast (e.g. Candida species), fungi and protozoa. Particularly they are used to control Escherichia coli, Pseudomonas aeruginosa, vancomycin-resistant Claim 3; Page 150; 167pp; English. AAYO9582
AAYO9582
AAYO9582
AAYO9582
AAXO9582
AAXO902
A

Enterococcus faecium, methicillin-resistant Staphylococcus aureus and penicillin-resistant Streptococcus pneumoniae. (A) are used to treat or prevent infections, in animals or plants, also as preservatives and disinfectants for medical equipment, foods, cosmetics, optionally as mixtures or in combination with other antimicrobials. Compared with linear analogues, (I) are more effective with better bioavallability and/or serum half-life (better resistance to proteolysis, allowing lower doses and making them more suitable for oral delivery). Since (I) are structurally related to naturally occurring antimicrobial peptides, they are less likely to induce development of resistant strains 88888888888888

Sequence 4 AA;

ö Gaps ö 0; Indels Length 4; DB 2; Le Query Match 76.2%; Score 16; DB Best Local Similarity 100.0%; Pred. No. 1.8 Matches 3; Conservative 0; Mismatches

1 RIP 3

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RESULT 13

AAY09580 standard; peptide; 4 AA.

AAY09580;

(first entry) 21-JUL-1999 Antimicrobial cyclic peptide beta-turn region SEQ ID NO:27.

Cyclic peptide; antimicrobial; amphiphilic beta-sheet; biostatic; biocidal; bacteria; yeast; Candida species; fungi; protozoa; Bscharichia coli; Pseudomonas aeruginosa; infection; preservative; vancomycin-resistant Enterococcus faecium; disinfectant; food; methicillin-resistant Staphylococcus aureus; medical equipment; penicillin-resistant Streptococcus pneumoniae; cosmetic

Synthetic.

WO9921879-A1.

06-MAY-1999.

97WO-US019557. 27-OCT-1997; 97WO-US019557. 27-0CT-1997; (INTR-) INTRABIOTICS PHARM INC.

Gu L, Chen J; Chang C,

WPI; 1999-312941/26.

Antimicrobial cyclic peptides with amphiphilic beta-sheet region.

Claim 3; Page 150; 167pp; English.

claimed cyclic peptides and peptide segments. (I) are broad-opectrum antimicrobials (biostatic or biocidal), effective against bacteria, yeast (e.g. candida species), fungi and protozoa. Particularly they are used to control Bacherichia coli, Pseudomonas aeruginosa, vancomycin-resistant Enterococcus faccium, methicillin-resistant Staphylococcus aureus and penicillin-resistant Streptococcus pneumoniae. (A) are used to treat or prevent infections, in animals or plants, also as preservatives and disinfectants for medical equipment, foods, cosmetics, optionally as mixtures or in combination with other antimicrobials. Compared with The present invention describes cyclic peptides (I): (i) comprising an amphiphilic anti-parallel beta-sheet region (A), a loop region (B) and a beta-turn (C); (ii) having net positive charge at physiological pH; and (iii) including at least one basic amino acid (aa) in (B) or (C).

AAY09554 to AAY09683 and AAY17301 to AAY17385 represent specifically

(first entry)

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Stable pharmaceutical composition comprising interferon compound(s) formulated for mucosal delivery to mammalian subjects in combination with mucosal delivery-enhancing agent(s).
                                                                                                        human; permeabilising; interferon-beta; IFN-beta; mucosal delivery; immunosuppressive; virucide; autoimmune disease; viral disease; multiple sclerosis; chronic hepatitis B; condyloma acuminata; papilloma virus; childhood viral encephalitis; wart.
                                                                              Human JAM-1 permeabilising peptide SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 4; 353pp; English
 ADG94025 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-122360/12
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                                                                                                                                                                                                           WO2004002404-A2
                                                                                                                                                                                 Homo sapiens.
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                                                      25-MAR-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Detecting autoantibodies from patients suffering from rheumatoid arthritis, by contacting a reactive peptide comprising citrulline residue or its analog with autoantibodies to form a complex, and detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for detecting autoantibodies from parients suffering from rheumatoid arthritis. The method involves contacting autoantibodies with at least one reactive peptide comprising a citrulline residue or its analogue for a time sufficiently long to allow a complex to be formed between the autoantibody and peptide, and detecting the complex. The present sequence represents a peptide of the
linear analogues, (I) are more effective with better bioavailability and/or serum half-life (better resistance to proteolysis, allowing lower doses and making them more suitable for oral delivery). Since (I) are structurally related to naturally occurring antimicrobial peptides, they are less likely to induce development of resistant strains
                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                  Rheumatoid arthritis antibody detecting peptide SEQ ID NO:91.
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                                                                                                              Length 4;
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                                                                                                             76.2%; Score 16; DB 2; Le
100.0%; Pred. No. 1.8e+06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                            autoantibody; rheumatoid arthritis; citrulline.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TEWE-) STICHTING TECH WETENSCHAPPEN.
                                                                                                                                                                                                                                                                   ADC13966 standard; peptide; 4 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-2001; 2001NL-01019540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-DEC-2002; 2002WO-NL000815
                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                         3; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                              Query Match
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Abd El- Shafy M;

De Meireles JC,

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The invention relates to a novel stable pharmaceutical composition

comprising one or more interferon (IFN) beta compound(s) formulated for

mucosal delivery to a mammalian subject in combination with one or more

mucosal delivery to a mammalian subject to more into more into macosal delivery to a mammalian subject yields enhanced mucosal delivery of

mucosal administration to the subject yields enhanced mucosal delivery of

the one or more IFN-beta compound(s). A composition of the invention has

immunosuppressive and virucide activity. The composition is useful for

treating autoimmune diseases, viral disease, for alleviating one or more

symptom(s) of multiple sclerosis (MS), chronic hepatitis B, condyloma

acuminata, papilloma virus warts of the larynx or skin or childhood viral

encephalitis in the subject without unacceptable adverse side effects.

The composition can be delivered intranasally which reduces or eliminates

compliance problems and side effects that attend delivery by injection.

The sequences shown in ADG94002-AD94810 represent permeabilising

peptides used in a composition of the invention.
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RESULT 15 ADG94025